

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCACTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAAGTGGTCGCTGCCATCGTAGG
ATTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCACTATGAGATAGTG**TA**ACCCAATGTAICTGTGGGCCTATTCTCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGTGA
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

1007527.12304

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLNNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTTIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAAGTCAGT
 GCCACAGCCCCGACCGCGTGTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
 GTTCCCTCTTTTCGGGGGTCTCTACCAGAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAAATCC
 TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGCTTGCTGTCTACTTTGTCTGGAATGTCTAAATGTTTC
 TGAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHLAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPFHEPRKKQNVDGLVLDLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

3007567-21-001

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGA
CAAGATGAGGAAGGCGGGAACCTAGGAGGCGTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATCTCTGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

101527-252101

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDYPYRQLREKDPKYSALRQNFRRYHGLSSLNLCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

AAATTACAGATTTTAAGCCCAATTCTGCAGTGGAAATTTTCATGAAGTACGACAGAGGACACCATCTT
CTTGATTATACAGAAGAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
GCTAGGCTCTTAATCCTCTGTGGTTTTCTGTGGACTCGTAAGGAAAACTAAGATTGAAG
ACATCACTGATAAGTACATTTTTTACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAAGCTTTTGATAAAAGGGATTTCATGTAATCGCTGCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGT
CTGATCAATAATGTCTGGTGTTCCCGCGTGTCTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGAGAGATTATTAATGCTTCCAGTTTGGAGGTGCGCTTGCA
ACCTGTGGAGGGGGCTATACTGCATCCAAATATGCACTGTGGAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAGCTTTTTGGTGTGACGCTCATGTCATGAACCAAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAACCTGCCAATTGGGAGCAGCTGTCTCCA
GACATCAAAACAACAATATGGAGAAGGTACATTGAAAAAGTCTAGACAAACTGAAGGCCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGAAAAAGATGCCAAAATTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGTGTGACTCAGCTAACACAAATGTCTCTCCAGGCTATGAAATTGGCCGAT
TTCAGAACACATTCCTTTTCAACCCCATTCCTATCTGTCCAACTGGACTCATTTAGA
TCGTGCTTATTTTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCATATAGGCAAGTCTGCCCTGT
ATTTAGGCTTTGCCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCAATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT
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AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
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ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGCGGGGGCCCCCTTGGGCCGTCGCCACCACT
 GTAGTCATGTATCCACCCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGAGCGTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGACGCGGAATATGATTCTCTTCTCCTTGGCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATGGAAAGCTCTGGCTTTACGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATGCTGGGTAAAAACCAGCAATCCACCCGCTTTACCAG
 CTCCTCAGAAGGGCGGACACCGACCTGAGAACTTACCTGAGATTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
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 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTCTTCTGCATGCATGGA
 AAGGATACCCGCAAGTTTGTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCTTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAAATTTAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAGGACG
 TGGACGTCAACCTGTTTGAAGACAGATCCGATCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTGGAAATCGGGCTAATGCGCTGC
 TCTCAGAACACCATCAAGATTCTTACTCGGATGTGGAACCTCGGATCTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTGAGCTGGAGTTCGGG
 GAGCTCTCCCGTCTCAGAGGGGATAAGAAGTTTCAGGAGGCGAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTCAGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACAGCTGCTGGAAGACTAGCTGGA
 AGCCATCGAGGGETCAGAAACGCACCTGCTGCGGCCACTCCGAGCCAGTAAGCTCACCTTTG
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTCGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCTGCCCGCCAGCCACATGGAGCTGGGCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCAGATCG
 TGCATTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTCTACCTGTACCGCCGTACAGGGGA
 CCGCAATACCAAGACTGGGGCTGGGAGATTCTGACAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGTGGCTTCTTCCATCAACAATGTCCAGGATCCTCAAGAGCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCTACGTGTTCACACCCGAAGCCACCTCTGCGCTATCT
 GGACCCCTGGC**TAG**GGTGGATGGCTGCTGGTGTGGGACCTCGGGTGGGCAGAGGACCTTG
 CTGGGTCTGTGGCATTTCGAAGGGCCACGTAGCACCGGCAACGCCAAGTGGCCAGGCT
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 GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCCTGCTTCTC
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 GAGGGGGGCTTCAGGTGGTGGCTGGTACTGGGTGACCGAGTGACAGCCGAGGGGTGCAGC
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 CTCAGAGGCGCTGAGGCTCAGGGCTGGCTCTGGTGTTCACAGCTGAGCTCAGGATCCTC
 TGGCGCCCGCCGAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCAGCGGCCCT
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FIGURE 10

```

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><subunit 1 of 1, 699 aa, 1 stop
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SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGQTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPLPPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFREL SRLTGDKKFQEAVEKVTQHIHGLSGK
KDG LVP MFINTHSG L FTHLG VFTL GARADSYEYLLKQW IQG GKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVDQPKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

```

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCCTGCCCCCAGAG
CCGCCCTTGAGCACTGGGAAGAACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCAGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC
ATCCTGTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
GCCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCCACCTGCATAGCCAGCCTGGCGG
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTC
AGC**TGA**GTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
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GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG
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FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
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GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFP EAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTCTGTGCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTATTAAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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FIGURE 14

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
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PRGEGEKVGDG
```

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCCCTCCGCGCCGCATAAAGGCTCCGGTCCGCGCTGG
 GCCCGCGCCGCTCTGTCCCGCCCGGGCTCCGGGCGGCCGCTAGGCCAGTGCGCCGCG
 CTCGCCCCGAGGCCCGGCCCGCAGC**CATG**GAGCCACCCGGACGCCGCGGGGCGCGCGCA
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 GAATTGCCGCTCTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTGAAGGAGACAGCTT
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 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTAAGAAAGACATGATTACACAC
 TGCTCTTGATGTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTCATGGAATTTG
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 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACCTGATGGTT
 GACATTGCAAGTAACTCATGTGTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG
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 GCAATGTTTCAAAATACATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT
 AAGACTATTACAGTT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAAATAACCTATTAT
 AAAGATTTTTTTTTGCGAGGAAGTAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACTA
 ACCAGGAAGAAGTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTTCCCTTT
 CTTTACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATATCT
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 GATTTTAAAGCAATAAGATGTTTTATGGGCCCTTAAAGTATCATGAGCCTTTTGGCAGTCG
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 TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAACAATATTTCCAGTCATTTTAAATGGC
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1001
 1002
 1003
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FIGURE 16

MEPPGRRRRAQPPILLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDPTLPNRTVTLILSNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTDFDYLASLSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDDPLELPSFYMT
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPEVVNNKGDFRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGFWADDDYSRCQYANDVTRVLYMFNQMPNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGTGTGMTCT
 VFQKVAASDRITGLSDYGRRDPEGNLDKQLSFKCNVSNFTSSIALKVCYIILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

1

GCCTGGGG**GATG**CTCTAGAGAGCTCGAAGGTGGTGCTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGA¹AAAAAGAAACATTCTGCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA
TCAT**G**ACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCTCGGTAGAAGCCCCATTAGG
TCCATGTCCAGTGCTTAGGGTGTGTTACTGAGAAGCACTGCCGAGCTGTGAGAGGAAGGGA
TGAGTAGTAGACTCCACTGATGACTGTCTGAGTCAGTCGGCATGTAGCAGAGCCACGAGAACA
TCGACCTCAGCAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

10017567-25/1001

FIGURE 19

CTGTCGCTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACAACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTGTGCCACGGCCGTTTCGCGGGACACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCCGGCCGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTGCCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTAGCCCATCTGCTTCACTCTAGCGGCCATGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTCTGCGGGCTGGCCCTTGCTGTC
 TGTCTCCTCTATGCCACCGCCCTTGTCTCTGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTGTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTCTCTGTTTTCTCTTCTGTCTCCCCCTCCCTCCACCTTTTTCTTTCTTCTCC
 CAATTCCTTGCACTCTAACAGTTCTTGGATGCATCTTCTTCCCTTCCCTTCTGCTGT
 TTCCTTCTGTGTGTTTTGTGCCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTCTGGGTTGCCTGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAGGTGCTGAGCTCACATCCACCCCTTGACGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAATAAATATATATATATAT
 ATTTGGAGGTCAAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGG
 CCCGCGCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAAATTTTGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTATCCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTTTTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFFVACI
IFAFISDPNLYQHQPAALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYYCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFEVKV
```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 22

MFLATLSFLLPFAHFGTVSCEYMLGSP LSSLAQVNLSPF SHPKVHMDPNYCHPSTSLHLC S
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES AFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDED FAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPSPRESAFRSLGLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTGTACACAAGCATACAGCCAGCCACCTAATTTGTTTCCCT
GGCACCTCCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTCTCTAATGCACGA
CAGATTCTTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTCCACATCAAGGGATTGTTATTCTTTTAAAAAAAACCAATACCAAAG
AAGCCTACA**ATGT**TGGCCTTAGCCAAAATTCGTGTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAAACACAGAACATTGCAGAAGTTT
TTAAACAATGAAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACTTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGCGGAGTCATTCCTCCTTTGAATCTACCCAACA
CAGCCACGGAATAACAGATTTCTCCAGTAACATCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAACTCCTGATA
ACAGTTCCATTACAGTTAGCATCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCTTA
TCAAGAAAAAACAACTCTACAGCCTACCTTAAATTCACCAATAATTCAAAACCTCTTTCCAA
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
GCTATTCTGGGTGCTCATTTGCTTACTCTTGTGGGTACTTGTGTGTGAAAAAGGAAAAAC
GGATTCAATTTCCCATCGGCACCTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCAGCTACTACAATCCAACCTTTGAAT
GATTCAGCCATGCCAGAAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTACTA
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCAGTGGAT
TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
TCACCATACAGCCCTGCCTCATAACTAATAATAAAAAATATTCCACCAAAAAATCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCATCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTCTTAATATATCTTAGGCTTCAA
TTATTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPI SLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTTLVGYL LCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSSYYNPTLNDSA
MPESEENARDGIPMD DIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTGTCAGTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGTTACTCT
 CTTAGGCCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCGTCATTACAAAGTACT
 TCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTG²CAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTGGGGAACGTC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCCTCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAAACTACTAACCACTGCAAGCTCTTGTCAAATTTTAGTTTAAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTGTTTGTTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTGTTTTGAACTTTTTGTGTAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTGCACTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGTGTGTATGAATTCTACAA
 CCCTATAATAAATTTTACTCTATACAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
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MVKIAFNTPTAVQKEEARQDVEALLSRTVTRQILTGKELRVATQKEGSSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSPFSDSDPAAIHDFEKGMTAYLDDLLGNCYLMPLNTSIVMPKKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNRKSFRLRRRDLGLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACACGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTGTACGCC
 AAGGAACCTGGTCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCTCCCCGAGCCTCC
 CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCCACAACCTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGTGTATGTTTCATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACACAGATGACCGGGCGGGGGCCCCGGGCCCTTCAGTGAGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAAGTCCA
 GGGACATGGGGTCCCACTGGAGACACCAAGGCGCAGGAGGACCGTGTCTCAGGGGTCTTG
 AGGGGGTGTGGTGGCGGTGAGGGCCAAGGGGAGCTGGAAGGCTCTCTCTGTAGCCACG
 GAAGCCCAGGGACCACTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG
 TGTCTAACAGTCTCTCCCGGTGCCAGCCTGACTGTGGGCCCCCAAGTGGTCACTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCTTGGCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTACAGC
 ACAGCTCCCTTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAATACTGCTCTTAATTTTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
 TCAAGCGCTCTCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAA
 AAAGA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSVPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

[illegible]

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESIGFRGQGVSSNMREISKEGNRLL
GGSGDNYRQGGSSWGSGGGDAVGVTNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

AACCGGTCCCTCGGGTCTCTGATGTGGCGATCTCTGTCGACGAGCGGTCGACGGCCGGCGGGTGGTCCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCTCTTGGTGCACATGTTTGTCCCTGTGGAAATATGACCGGCATCTTCA
 CTCTCTGCTGCGCTGCACCCGGAGTTTGGTGTCTTGCAGAGGAGATGAGGGGAATGATGTGTTTCTTCCGAACAAGC
 TGCTGTCTATGTCTGCTGTCTGGGCTGGCTTTTCCAGATTTCCACACAGTCCTGAGACATGTGTTCTTGGAAAGCT
 GTCCTCTATATGCTTTGAGGTGGACACAGTAGCCCGACGAGCATGCTTGGACAATGCSCCTGTGCTGGACACCG
 AGCTGCTCTACACCTGTGCTCCCTACATCGGAGAGCTCCGGAAATGCTCGCTCTGTGGGTGTGAGGCAGTAGTG
 GACGAGGATGGGGGGTCTCATGAGGAAATACACCCACCACTACCACAGCCTGGGAGCGCCAGCCTTCCGAGACA
 CGCAGGGGTGTCGAGCAGACAGCTCCGCCAGGGCTTTTCCACACAGCCGCCCTCTGTGGCGGCGACCGCTAGAG
 TCGTGCGAGAAAGAAATGGATCAAACTGTGTCAAACTATCAAGGTACACTGTTGGCGAGATCTGGTGCCGACG
 CAGAGTCACTTCTCCAAAGCAGCTGTGTGACACAGGGAAGGAAGGGGAGACCCAGCCAGCAGCTGTTGGAGATC
 GTGTGTTCCGAGCTCTGCCCTCAGCGGGCCAGCAGTGTGCCCTGGGGGGGAGTTTCTGTCAAGAAGAGCCCGTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGAGACCCCGGACCGCTTCTGAGCAGTGCAGAGAAATCTGTTGTGGGCG
 TTGCAACAGAGAAGAGCTGTGCTTGGCTGTGACCGAAATACAGCACTGATCAGGAGGGAGGTGAAGACAGGAG
 TGAGTGCACATCTGACGCGCCAGGGTGTCTGAACTGCTGTCGCGGGGGGAGCGGGGGCTGTCCCGCGCTCGAC
 TGCTCTCTCTTGGCGCTGGGGCGACCGGACCTGACGAGGAGATCTCCCGAGACATCTGGAAACAGCTTCTGAGT
 CAGCTGGGCGACAGCTCGCGGTGCGCGCACTTCTGTGCCCACTCTGACGAGCATCTGGCAAGTGTCTGTGTG
 TGCTAGTCTCTCTCTGCTGTGAGATCAAAATCTATCTAGGGCCCGCCGACATCAGAGCTGAGAGAGGGG
 CAGGCTCGAAGGCTTTGACATGCTGCTCTCTTGTGGAAGAGAATCTTTCAGGGCGCGTTCGCGTGCAGCTGT
 CTCCTGAGCGCAAGAAATGTGGGCTCTCTGACAGCAAGGCCAGGAGGTGGGACTGCTGCTATTTCTGTCTA
 CGGGAGCTGTGTGGAAGAGCTCTGATGGGACGAGTGGAGTAGAGGCTCTGCTGGGACGCTCCACGAGGCCAG
 TGCGCAGGGGACTTGGCTGAAATATGACCAACTGTCTATCTGTACGGCAGGCCACTGATGCCAATGACAGCCCTCA
 CAGCTAAGAGCTGTGAGTTGGTGCAGCCAGCCGGGCATGTGCTGGCCAGAGTCTAGGGCTGAGAGTGGCC
 CTGCTTTGGGCAATGCAACAGAACCTGGACCCCGGCTCACGAGGACCCAGCTGCCAATGACAGCCCTCACT
 TGTTGGGCTGAGCTGGGTCTGAGTGCAGCTCAGACTCTCTGCTTAAGGTGTCACTCTGGCATCCCAACCGGGA
 ATCTTAGAGGAAGAGAGTGTGGCTCTATTTGGGATATGGCAAGAGTCACAGATGCGAGTCTGTGGATAGAA
 GAGGTGGTTGTGTTATCTTGTGATCTTGGATACTAAATGAGGTGTGTGGGCTGTGCAACAGAAATCAGGCTCT
 CATTGCTATCCGAGCATCTTAAAACTTTGAGTCTTGAATATCATGACAGGAAATGACTCTGCTTAAC
 TTATGAGAGGCTTAAGACATGAATCTGGAGTCTACATTTCTTATACACAGGAGCTGGACTGCCATCTCTT
 ATAAATGCTTAAACAGCGCGGGTCTGGTGAGCTCATGCTGTATATCCGACATTTGAGGCTGGCTGCGGCG
 GAGCTCGTGAAGTCAGGAATTCAGACAGGAGCTGGCCACATGTCGAAATCCCATCTCTACTAAAAATAAAAAA
 TTATAGTGGGCGATGTGGTGTGTGTGCTCTGTATCCCGACTCATCAGGAGTATGGCAGGAGACTGCTGTGAAC
 CTGGAGTGGAGTGTGAGTAGGCGAGTGTGCAACCATGCACTCCAGTCTGGTGAACAGAGCAGACTTTCTAG
 AAAAAAGCTTAACAAACAGTATAGGTAGGACTCAACCACTGAAACTGACTTTCCCTCTGTATCTACGCCCCGT
 TCGAGTAGTAACTCTTGAGCACTCTCCCTGACACGGGACAGCAGCAGGCAATTAGAGCTTTTAGAATAAA
 CTGTTTCTCTTTAAAAAATAAAAAAAGGGGGCGGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAATAATCTCCCAACAGATGGCTCTGCAATCTGCACAGCTC
 TGGGGCTGTGCTGTAGGAAAGGCCCTTTGCTTCCCTGAGCGGGCTGGGCTCTGATGGGTCTCGCGAGCTG
 GCGTGCTTGGCGCGCTGGCTGTAGCTGTCTTCTTGGCGGACAGAGCTGCGGGTCTGGGGGACCCGGG
 AGCTAAGGACAGGCTCTGTGTGAGGGTGGAGCTGCTGTCTTAACCAACCTGAGGTGTGCTCTGAGTGTGCTG
 GGTGACCTGTAGTGGCAGGGGAGCAGCTGTGGCGGTGCTCTCTYTAGGCCACTCTGGGAAATAGTCT
 GGGCCCTCTTCTGAAGAAGCAGGATGGGGTGGGTGTGGGGGACTCATGGGAAATGCTCTGAGGAGTCACTGT
 GAGAGGGGGCGGGTTTGTGGCTGCAGCGGGCTGAGCGCTCTCTCTGAGCTCATGTTCCCTTCCGTGTCT
 ATGAAGAACTCGGCTCTGGTGTCTAGGGCTATAGAGTCTGCCCTCAGGAATGGGCTTGGACAGGCTCATGT
 GTATATTTCAACAATCTCTGCGAGCTGTGGCTGGGCACTCATGGAATGGCCCATGTCCCTCTGCTGCTGGAC
 TGTGCGGCTCGGAGTGGCGACAGCAGGCGGGCGAGAGCTGGGCTGGGGTGGAGGAGGCGCCCGGGAGG
 CCTCAGGAAGATGGGCTCCGCGACACGAGGACGGGCGGGCTCCGCGCGCGCCGCCACACCTGTCAGG
 GCGGGTGTAGCAATGGAGATCGGCTTGGGCTCGCTGCGCAGAGTGAAGCTTGTATGCGAGTGGCGCAGCGG
 TCTGCGCCAGCTGGAAGAGCGGCCGCTGCACAGCAACAGCGCTGCCCT

FIGURE 32

MCFLNKL L L L L L A V L G W L F Q I P T V P E D L F F L E E G P S Y A F E V D T V A P E H G L D N A P V V D Q Q L L Y T C
 C P Y I G E L R K L L A S W V S G S S G R S G G F M R K I T P T T T T S L G A Q P S Q T S Q G L Q A Q L A Q A F F H N Q P P
 S L R R T V E F V A E R I G S N C V K H I K A T L V A D L V R Q A E S I L L Q E Q L V T Q G E E G D P A Q L L E I L C S Q L
 C P H G A Q A L A L G R E F C Q R K S P G A V R A L L P E E T P A A V L S S A E N I A V G L A T E K A C A W L S A N I T A L
 I R R E V K A A V S R T L R A Q G P E P A A R G E R R G C S R A

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TTCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTTCTCGACGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCAGGGCCACTGACAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
 AGTAGCAACAAGAGCAGCGGTGACGAGTGTTCTGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCGGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGGTATGTCCCCATPTCTCGG
 AACAGACACTGCCCTCTCGGTGCCACAGTGTTGTATTGTGACGAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGTGGCCATTCC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCGAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCCAACATGGAAGCATATGCCGTCTCTCCGCGCGCATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTGCTGGTT
 GAGCACAGGCTGGTTTACCATTGGTGATCGCGGTGGAGTTGTGTGACCACTGCATGTCTATG
 GCATGGTCCCCCCTAATCTGACGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCCGAAGGG
 CAACCCACCCGCTTCTATCACCAGAGAAAGGGTCTTCTCATCTGTTGGGCCCATGATGGCA
 TCACCTTCTCCCAACCCCTCTCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCGCAGCCGTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGCTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCACTCAGGGCTGCGGCACAGTCAATCAGGGTAGAGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTTG
 CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGGACAAACCCCTCCCCCTCTCTGGG
 CACCCCTCTGCCACACCAAGTTTCCAGTGGGAGTCTGAGACCCTTTCCACCTCCCCCTACAA
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTCG
 GCAAACCTCCTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAGGGCCAGGCCTCTTTCTGCGCT
 CTAGCAGGAGGTTTCCAACTGTTGGAGGCGCCTTTGGGGCTGCCCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCGAGGGTCTCCCTCGACCTCTGTGCTCTGGGATGGCTGTCTGGGAGCTGT
 ATCAGCTGGGTTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCTCAGTGG
 GGTGTGTTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTGGTTTTGTAATGATTGTACAGCAATAAACACCTACCTACGC
 TCCGGA

1007562.121301
 1007562.121301

FIGURE 34

MSSNKEQRSADVILFALITILILYSSNSANEVPHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFRVLRRPQEFVNRTPETVFIFWGPSPKMQKPQGS�VRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPLQRMPIH
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTGGCGTCTCTAAAGGAAAAACACTAAATGAGGAACTCAGCGGACCGGGAGCGACGAGCTT
 GAGGGGAGCACTCCCTACTGTTGGCCGAGAGGGGCGAGGCTGAAGCCCGAGTGGCCCGAGGTTGCTTGAGGGCGTGG
 GCGAAGGTGAAGAGCTTTTCAGCAACAGCTTCTCGAAGCCATGACCCATGAAGTCTTGTGCAGATTTATACCGT
 CTGAGGGTAGCAGCTCGAAACTGAAGAAGTGGAGTGTTCAGGAGCGGCAATCTCTTTGTGTGGTCCCTGCG
 GGCTATGCGGACCTTGGCTTCAGACCTTTGTGATACACCTAGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGCCCTGAGGTCACACTGCGCTTGCCTCCTCTAGCCACAGCAGGCTGCTTTGCTGACTTTGAACGAGGTCCTCAG
 GTCAACGCTCAGGCTGCGCTCCACGCTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCCA
 AGGATGAATGTAACTCTGGCGCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCTCATCACC
 CAGGGACCTCGTCTATCACTGCCCTTAACAACCACTACTGGGACGCTACCAAGTGTGGCCCGGATGCTCGCG
 GGGCTGTGGCCAGCGTGGCAGCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGTGTGCAGCACTGTG
 ATTGAAGTGGATGAGGGAACACAGCAGTCTATGCTGCCACTGCTGAGAGCCACCCAAAGCCGAGTCCGGT
 TACAGCGTCAAAACAGAGTGGCTGGAGGCCCTCAGAGGTAACTACCTGATCATGCGCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTTACAACCCAGTGAACCCAGGAAGTGAAAGCT
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCCTGAGGCTGCCCGCATCATCTACCCCGACAGGCC
 CAAACCATCATCGTCACCAAGGCGCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGAATCCACCCCGACGGGTC
 ACTGGGCCAAGGATGGGTCAGTGTCAACGCTCAACAAGACCGGCTCTCTGCTGAGCAACCTCTCATCGAC
 ACCACCGCAGGAGGAGCACTCAGGCACTACCGCTGCTATGCGGCAAGTGGGTTGGCAGCCCGGCGAGCGCT
 ATCTCTACAACTGTCCAGTGTGTTGAACCCCTGAGGCTACCATGAGCTATCCCGAGTGTGCTCTCCCTCGGCG
 CAGAGTCCCAAGCTTACCTGTGAGTGTGGGAACCCCGCGCCTCCGCTGTGTGGTGAAGAACTGTGTGCC
 CTCTATCTCAGCAGCGCTCTCCGCTCTCCCGAGGGCCCTCGCGTCTCAGCATGGGCGCTGAGGAGGAAGG
 GTCTACCACTGACTGGCAGAGAGGTTGGGAGCGCCCATGCGGTAGTCAGCTGGGACCTTCAGGCCAAGC
 ATAACCCCAAGGCTATGGCAGATGCTGAGCTGGCTACTGGCACACTCTGTATCACTCTCCAAACTCGGCCAGC
 CTTGAGCAAGTACTGGTGGGCGCAACCGGCGCTCCCGAGACCTCACTGGGCGCTCTTCTCCCGAAGGTG
 CCGAGGAGAGAAGGGGAGGGGCTCCCGCGAGGCTCCCATCTCTCAGCTCGCCCGGCACTCTCAAGACAGAC
 TCTATATGAATGTTGTGGCGGCTCGCATGAGGGCAGTGGCCGGCGCCCAATCTCTATATGTGGTGAACAC
 CGCAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCAACACAGCAGCGCTGACCCCT
 ACCAGACTTGACCCCGGGAGTTGTATGAAGTGGAGTGGCAGCTTACAACGTGGCGGAGAGGAGGCCAGCAGCC
 ATGGTCACCTTCCGAAGTGGACGGCGGCCAAACCCGAGATCATGGCCAGCAAGAGGAGCAGATCCAGAGAGAC
 GACCTTGGAGCCAGTCCCGAGGACAGCCAGCCAGCCAGCCAGCCCGCCTCTCCCGCCCAAGAGCTCCGACAGG
 CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGCTGGGAATGTTGGTTCCTCAAT
 CAGTCCCTTCGTTGGAGTACAAGAAGCTTAAGAAGTGGGAGACTGGATTCTGGCCACAGCGCCATCCCGCA
 TCGCGGCTTCGCTGGAGATCAGGGGCTTAGAAGGCGACTCTCTACAAGTTTCAGTCCGGCTCTGAACATG
 CTGGGTAAGAGCTCCAGCGCCCTCTCGGCGCTTACGTTGTTCGGGCTACAGCGTCCGCTGTACGAAGG
 CCGCTGCCAGTCTTATATCACTCTCAGGATGCGCTCAATGAGACACCACTCATGCTCAAGTGGATGTACATC
 CCAGCAAGTACAACAACACCCCAATCCATGGCTTTTATCTATTATCGAACCCAGACAGTGAATGATGATG
 GACTACAAGAAGGATTTGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACTGCAGCGAGACAGCTCCTAC
 GACATTAAGATCGAGTGTCTCAATGAAGAGGGGAGAGCGAGTTCAGCAACGTGTGATCTGTGAGACCAAGCT
 CGGAAGTCTTCTGGCCAGCTGCTGGACTGCCACCCCAACTCTGGCCCCACACAGCGGCCCTCTCTGGAACC
 ATAGAGCGGCGGTTGGGCATGGGCGCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGCTGTG
 CTGGGCTCATCTGTTCTCATCTGCTCACTTCTATCCCTTCTGCTTGTGGAGGCGCTGGTCTAAGCAAAAACAT
 ACAACAGACTGGGTTTCTCGAAGTGGCTTCCACCTCTCGGCCGTATATCTGTTGCTTGGTGGAGGACT
 CCAGGCCACAGGCCAGTGGCAGCCCTACCTCAGTGGCATCAGTGGAGCGGCTGTGCTAATGGATCCACATG
 AATAGGGGCTGCCCTCGGCTGCACTGGGCTACCCGGGCACTGAAGCCACAGCAGCACTGCCCGGCGAGCTTCAG
 CAGCAGGTTGACACCAGCAGCTGCTGAGCGACGCCCATCTGGACTGGAATGCAATGACCCCAAGTCAACGATC
 ACGAGGGTCCCAAGTCTAGCCCGGAGCAGGGCTCTTCTATACACTGCGCCAGCTCTGCTCAACCTCTCACT
 CTGCGGCCCTPACGACTCTGCGCACGCCAGGAGGAGGAGCTGCTGCGGCACTCAGGGTCAAGGAGGAGG
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 CTCACATTTAGGCAAGAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAGAAAAA
 AGAGACAGAGAAATGTTATTTTCTATTATAGCCATTTATATATTATGCACTTTGTAATAAATGTA
 TATGTTTATATATCTCGAGAGACATAAGGAGTCTTACCGTTGAGGTTGAGAGAGGAAAAATAAGAGTCCGCCA
 CTTAAGAGGATCACCCAGAGAAACACCCGACAGGCTGGCGGGGACAGACTCTAATCGGCGCTCTGCAATG
 CGAGGCGAGGCTCGAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGCGAGATGGTTCATCAGAGCA
 TGAGGGAACAGCAGAGGGGACGGTATCACAGCTGGAGACACCCACAGACAGATGGCTCGGTCACGGGAA
 CAATTTTCTTAAGATGCCATGAGAACAGCCAAAGATGTGTACAGCATATGAGCATTAAGAAATCTCCCAAGT
 CATAATCTCGGCACATATCTCTAATAAACAAACACTGTAACCTTAATAAATGTTTAGTCTTCCTCGTGAATA

FIGURE 36

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQASTVQKPGGTIVILGCVVEPP
 RMNVVTWRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQT IIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTS EEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPEVTMELSQLV I PWGQSAKLTCEVRGNPPPSVLWL RNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEEKGQAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFP IQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMI IPASNNNT
 PIHGFYIYRPTDS DNDSDYKKDMVEGDKYWHS ISHLQPETS YDIKMQC FNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAWSKQKHTTDLGFPRSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYD PQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSFVLEAVWD PPFHSG
 PPCCLGLVPVEEVDSPDCQVSGGDWCPQHPVGAYVGQEPGMQLSPGLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCATTGTGGGCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCTGTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTACTACCCAGGCTCACTAGCCAGG
 CACCCCCAAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCGAGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCTCCTACTCTGAACCTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCACCAAGTTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGAAATTATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAATGCCT
 CCCCATACCTTGTTCAGGCCCTGTGGCTGCTGCCACCATCCCAACCTTCACCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGA AAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYGQLSTSCH
SHLVFPQNGHQATHLEVTKQFTNRVPPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCACGAAGCCTGATAAGCATG
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCACAA
GAGTTCGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGAGCCCATGCC
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAACACAGTCTCGAGCGTGTGGAAGGTGCCCAGCAGCGGTGAAGATGCG
AGGTGCAGGAGCAGCGGAAGACAGCTCTTCGATCGGCACAAGATGCTCAGCTAGATGGGGTGG
TGTGGTTGGCTCAAGGCCCAACACCATCTGCATCGCAGCTTCCAGGCTGGACAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTFCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGTCTCTTCTGCAAGT
GTTCTTATACCACTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCCACTGGGTCTTCAGGGTGCAGTGGA
AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCAAGTGT
CACAGTCACTGAGCCAGACGGTCTGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGACAGGATGCATGGA
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAGGAAGCCATCATTAATTTG
TTTTATTCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEFM
FVPGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

ASGCGGCTCTCGCTTGGGTTCGCTAAATTTCTGTCTCGAGGCGTGAGACATGAGTTCATAGGGCTCTTGGGTCCCGGA
 ACCAGGAGAGGTTGTGGGGAGACACATCTGCAAGCCCTCCGCGACCTAGGCTGAGGCGGCGCTGTGGGGTCTCCCT
 TCCGTTTGCAATTCACACCCCTCCGGGCTTTGGGCTCTCTCGGGAGCCCTCGCCGGGAGATGGCCGCCGTGTATG
 CGGAGCAAGGATTTGCTCTGCTGCTCTCTCTCTGCGCGCGGTGCTGATGTGTGGAGAGCTCACAGATCGGCACT
 TCGCGGCGCAAACTCAACTCATCAAGTCTCTCTGCGGCGGGAGACGCTGCTGAGCGGCCCACTCATGATCTCGG
 GGCATGTACCAAGGACTGGCATTCGGGCGGAGTAAAGAAAGGAAAACCTGGGCGAGCCGTACCTTTGTACAGT
 TATAGAGGATGTGAAGTGGAGGATTTGGCAACAGTCCCCAACGAAGTCACTCGGCTCATGCTGGTGTGCGGAGA
 AAAAAGAGCGCTGCCACCGAGATGGCATGTGCTCGGCAAGTACCCTGCGAATTAATGGCATCTGATTCCTCAAGT
 ACTGAAAGCATTTTAACCCCTCACATCCGGGCTCTGCTGGATGTGACTCGGCACAGAGATCGAAACCACGCTATTAC
 TCAAAACCATGACTTGGGATGGGAGAACTTAGGAGAACACACATCAAGATGTACATATAAAAGGCGATGAAGGA
 GACCCCTGCTACGATCATCAAGACTGATTGAAGGTTTTGCTGTGCTGCTATTTGCGAACAAATTCGACAA
 CCAAGTCTCCATCAGGGGGAGTCTGTACAAACACCAAGAAAGGTTTCATGGGCTGGAATTTTCACAGGT
 TCGCATCTGCGAAGGCCGTGTTCTGCAAAAGTAGAAAGATGCCACTACTCTCTCGAAAGCCAGACTTCAGTGTG
 TGTGAGAAAATTTGATACCACTTAGGGAACATCAATGCTTCGACAGTGTGAAGTTGTGATTTAATGCATATTAG
 CATGTGTGAAAATTAGGTTGAGATCGAGAGAAATGCTAAATAAGAAACCTGATAAGCAATATAGATGATACAG
 AARGGGAGAAAGAAACATGAACTGAATAGATAGAAATGGGTGACAAATCGATGCGCCAGTGTTCATATTG
 CAACCTTGCTCATGTAAATAATGTACACATTTGTGAAAGTGTATTTAATGAAGAGAAACGACACAGTGGAAAT
 ACTGATGTAGTACATGTGACTTTCCAAAGTTTGTGGTTGTGTGGAGAGAGGTTTCCTCAGAGTGTGATGTGCT
 TTATACAAATAACCTCATCGAGATTTCTATTCAACGTTAGAGTTTGACAAAAATCTCTGAGATTAACCTTGTTA
 TCAAGTAGGTTCTAAAAATAGCAATTTGCTAAACAGAAATGAAACATGAGCAATTGTAATTTACACAGAAAT
 TACCTTTGATTTGTAAACACTACTTCTGTGTTCAATCAAGACTCTTGATGATAGAAAATAAATCAGTCAATAT
 TCCAAATAATTCGAAATTAATGGCCAGTTGTGTAGGAAGGCCTTTAGGAAACAAATAATACAAACAAACAG
 CCAACAAATACITTTTTTCAAATAATTTAGTTTAACTGCTAATTAATGAAGCATGATACAGAGCAAAAACAGTCTG
 TCGAGTTCTACGGAATGACGATATCTCTCTTTATCTTATGTGATGCTCTGCTGTAAGTCAATATATTTCAC
 AACTATTACCAATAAATTTGTGACTAGTAAATATCTACACAGAGCAGAAATTTTCACAGATGGCAAAAAAATTTAA
 GATGTCCAATATTTGTGGGAAAGAGCTTAACAGAGATCATTTATTTCTAAAGATTGGCCATACCACTATTTT
 CATGATATTAGATTGTAATAATCATGTTATCATACATCTCTCGGTTAAGAGACTTAGCTGGATCTGTACTG
 CACTGGAGTAGCAAGAAATTTGGGAAATTTTTCTGTTGTCAGTTTGGCAACATGACATCATGTCTG
 AGGCAACAGTTTCGCTGCTCATCTTTGAAACCGAGGGAGTCAGACTTAATTAATATTCGATCGGATTTGCTAT
 CATATAATTTACATGACAGTAATTCAGTGTGAGTCTGTGCTGATCTCTCAAAATTTCTTAATTTATTATG
 TGCTGAGATCTCTAAATAATCTCAATTTTCAGGAGGTTTCCAAATAATGACTCTCTGAAGTACAGACAGTGTGAGG
 TTTCAATGGCCCTCTATAGCTCTGACTAGCCATGGCATCACTAAATTTCTCCAAACCTTCGACGACTGT
 TCTTTATGGCCAAAGGCTAGTTTCGGTTTTCTGACGCCATTGCGGTTAAAAAATATAGTAGGATAACTGTGAA
 AACTCAGATATGCTAATCTATAGACACACAGTCTCTAAATTTCTTGAAACCAACTTACTACTTTTTTAAACT
 AACTCAGTTTAAATACTTTGCTGGAGCAACAAACAAATAAAAGGTTTACTTATAGTCTGGACTTTAACTTTG
 TAGACACAAATCTACTTTTGTAGTTTCTTTTACTTAAATCCATCTCGAGTCTCAAATTTAAGTCTCCCGTAG
 AGATTGAGTTGAGCGCTATATCTATTAAAAATTTCAACTTCCCATATATTACTAGATGATTAAAGACTTA
 CTTTCTGCGACAGCTCGCAAAAAACAAATTAATAACTAGTCCATCGCAAGAACAAAGTTTGTATAAACAGGT
 TGCTATAGGTTGTGAAATGAAATGGAACATTCAATCAACAAATTCCTATATAACAAATTTATTAATTTTCAAT
 TTGGTTTTCGCAATTTTCTTTATGTCCACCTTTTAAAAATTTATTTATGAAGTAATTTATTTACAGAAATGT
 TTAATGAGATGATTTTCTATAGAGATATTTCTACAGAAAGCTTTGAGACAGATATTTTTCGACGATTTGAC
 TTTGTAATTTAGGAAAAATGATAATAAGATAAAATCTATTAAATTTTTCTCTCTATAAACCTGAAAAA
 AAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGYSNHDLGWQNLGRPHTKM SHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

ICTCAATCTGCTGACCTCGTGATCGGCTGACCTTGTAACTCACCTACCTTTGGCCTCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCAGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTGAGATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTCTTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCTCT
 CTGTTTGGAGTCTCTTCTTCCAGGCCAAACTTCGAGAATCAACACCTGGAGAGCATCC
 CTCCACTGTGAACAAGCTTTTTCAGCTTCCCAAGCAGCAGATGAAACATCTCTCTGTGTCG
 TCCACCAGCCACAGGCCAAACACATCAAACCTTGCTAAGCGCGGATATCCCCAGCTTCTAAG
 ATCCAGCTTCTGCAAGTGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCACTT
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTTCCATCAGCTTGTTATCGAAGCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTATTACCTCCTG
 CAGCTGCAGAAGCTCATCACTGAATTCGTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGTCTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTGCATGGCTGGTGCCAAACCAAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCGT**TAA**AAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTTCTTGCCTTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTTGGGCAACATGGTGAAATC
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGGGAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQKRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

CCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCTGCTT
TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCTCTGCACTCAGCGGTGGAGGAGACGG
ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTTGCC
GTCGCGCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA
GGTGCTGGCGGTGGCGCGCGGCACCCGCGCTTCTGACCTGCGTGAAACCGCGGCACGTGT
GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG
GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA
CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCTGCCACCTGCAC
CACCATTACTGTGGCTGCGACGAACGCGCGTCTTCCACCTGACGGTCGCGGAACCCACGC
GGAGCGCCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCACG
ACCCACACTGGCGCGCGGCCACAACGTCATCAATGTCACTGCCGAGAGCGCGAGCCAC
TTCTTCCAGCAGCTGGGCTACGTGCTGGCCAGCTGCTGCTCTTCACTCTGCTACTGGTCAC
TGCTCTCTGTCGCGCGCGCAGCGCGCGGAGGCTACGAATACTCGGACCAAGAGTCTGGGAA
AGTCAAGGGGAAGGATTGTAACCTTGGCGGAGTTGCTGTGGCTGCAGGGGACAGATGCTT
TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
GCAAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCT
CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCGCTTTCCT
GGAATTGGCCTGGGCGTATGACAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
AAAATCCCACTGATGCCATCATGCCCTCAGACCTTCTGGGCTCTGCCGCTGGGGGCTG
AAGACATTCTGGAGGACACTCCCATCAGAACTGGCAGCCCCAAAACCTGGGGTCAAGCTCA
GGGCAGGAGTCCCACTCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCCT
CCTCTGGGGTGCTGCCGCCACAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCCTAGCCTTG
CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCT
GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
CAGGGGAGGAGTGAAGTTGGTTTGGGGTGCCCTGTGTTGCCACTCTCAGACCCCAATTT
GACTCTGCTGGTGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVIDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRVVEAQVHVHWDQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGDGDFSLRIEPLLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPFPPRGSPNGSSHSGAPGPDPTLARGHNVINIVIPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLKGFRENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGCGTGGCGCAGCGGCGACATGCGCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACACGGAGGC
 ACTGCTTGAGAAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
 GGACCCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGGCTCCACCG
 TGCCCTCCATGCTGTGCTGGTGGCCAACTTCTGCTGTGCAACAGGGTTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCTGGCCATCTTCATGGTGATAACTGCATGGTGAA
 GGTGGACACTTCTCTCTGGACCGTGGTTTTTTTTGCGGTACCAATGTCTGCATGGTGATCC
 TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCTGCTGTCTGCATGGGACTCTACTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCTGTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTCAATGATCCCAACACCCCTCTCC
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGCACCTACGCTCTTCTTCATACC
 AGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACCTTTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCACGGG
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTTCTCGTCTGTGTAACACAGCCCCGGGT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCTCAGCTCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTACGCGCCCTAAGATTGTGCCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAAGGAGGACACAGGACATTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGAGGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCAGCTCCATGCCATTCCGTGCAAGGCAGATATCCAGTCAATATTAACAGAACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCACCTTCTTTTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTCGCCTCATTCAGCT
 GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCAGTGGTCACTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAACAACCTGCCACTAACAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGCTCAAGATGAGGGTC
 TTTAGTGTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAACTTGC
 GTATTCAAAA

4017527.121304

FIGURE 48

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYYIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSVA SRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPAVCTNIESLNKGGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELA EATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPPEKLGALRPQEKGHSPEDIYQMA
LNQALKDKLALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLDVMSDEGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPLRALSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPPLPRHMQEALRRLHYVPATKVFLSFRPPFWREEHIEGG
HSNTDRPSRMI FYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVA SSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GAGCCTCTGAAAGCCACCTCTCTCTGGAGGAACACGAGCGAGGGGAAGAACAGGACAGGACTCGTGTGCAGAGAA
 GAACCTCAGAGCCGGGAAGGCCCAATCTACTAGAAGCACTGAGAGATGCGGCCCTCGCAGGGCTCTGAATTTTCCT
 GCTGTCTGTTTACAAAGATGCTTTTATCTTTAACTTTTGTCTTCCCCACTCTCGACCCCGGGCTTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTCTTTGTGGCTGATCACCAGACCTCAACCCGCTCTTACCTCTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTTGAGGGAGGACGACGGGAAGGGGTTTCCCAAGAAACAATGACCTTAAACAAGTTGCTG
 CTCTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTCTCTGACAATGGGCCCTGTTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGACAGATACCTGGGTTCT
 CTCTCTCTTGCATAAAGGTTATAAATCATCACCAGACCACTTTGTGGCATCTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGAAGC
 CATCGTACATATTTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAGGCAATTTGGTGCTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCTGAAGGTGATCATCCTTATGAGCACTTGTGATGATGACCTGAA
 GCAAGAGGGGGAGAAGTGAATTTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGCACTTCAAG
 AAAACCTGTGCCTCCTAGCCCAAGAGCTTGAAGGCTCATCTGCTTCAACAGTGGGACCAAGGTGACCCCAAGG
 AGCCATGATAACCCATCAAAATATTGTTTCAAAATGCTGCTGCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGATGATGTGGCCATATCTTACCTCCCTCTGGCTCATATGTTTGAAGGATTTGACAGGCTGTTTGTGTA
 CAGCTCTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTTCCCGGGTGCTCGACTCCTTAAACAGGATCTACGATTAAGGTACAAATGAGGCCAAGACACCTTT
 GAAGAAGTTCTTGTGTAAGCTGGCTGTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCGATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAGATCCAGGACAGCTGGGCGGAAGGTTCTGTGTAATTTGTCATCTGGAGC
 TGCCCCATGTGCCACTTCACTGATGACATTTCTCCGGGACGCAATGGGATCAGGTGTATGAAGCTTATGGTCA
 AACAGAATCCACAGTTGGCTGTACATTTACATTTACCTGGGACTGGACATCAGGTGATGTTTGGGTTGCCCTGGC
 CTTCGAATTTAGCTGAAGCTTCAAAGGATCTGAAGGACCTGACAAGACAGCAAGAACCCCTGGACATGATGGCTG
 CAGGCTGAGCAGGAGACATTTGGTCGTGGCTCCGGAATGGAATCTGAAGATCATCGACCGTAAAGAGCAATTTT
 CAACTGTGCGCCCAAGAGATACCTTGACCCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCACTGTTTACA
 AATTTTGTACACGGGAGAGCTTACGCTCATCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTCTCCCT
 ATTTGACGCAAGGCTTGGGGTGAAGGGCTCCTTTGAGGAAGTGGCCAAACCAAGTTGTGAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAAATTTGGGAAGAAAGTGGCTTAAACCTTTTGAACAGGTCAAAGCCATTTTCTTCTATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAGAGGAGAGCTTTTCAAATACTT
 TCGGACCCAAATTTGACAGCTGTATGAGCACATCCAGGATAGCATAAGGTACTTAACTACCTGCCGCCCACTG
 TGCATGCTTGTGAGAAAATGGATTAAGAACTATTCTTACATTTGTTTGGCTTTTCCCTCTATTTTTTTTAAAGC
 TGTAAACTCTAAAGCCATAGCTTTTGTTTATATTGAGACATATAATGTGTAACCTTAGTTCCTCAATTAATCA
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCTCTGCTTCAA
 GATCCAGTTTATGTCTGTGCTCTCTCATGATTTCCAACTTAATACTATTAGTAACCAAGTTCAAGGGT
 CAAAGGACCCCTCTGTGCTCTCTTCTTGTGTTTGTGATAAACATAAATGGCCACAGCTCTATGCTTATTTTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTTCTGAAAACCTGCTTACAATTTATGTTTTCTAGCCACTCCAC
 AAACCACTAAAATTTTGTGTTTGGCCTATCACTCATGCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAATTTGTGACTGAAGGGAAAGTTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAAGTTTGGGCTCTATGACATAGTCTTCCAAAGGAAGTGTGTTCTTAAAGCATTTTAA
 CAGTAGGAACTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
 GGTGGGCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGAACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGGATT
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTCTACTGTAAATGTAAAGTCTTTAAATTAAC
 TATTACAGATAAAAA

10017327-12331

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLFTKMLFIFN
FLFSPPLTPALICILTFGAAIFLWLITRPQVLPDLLDNNSQVGIEGGARKGVSKQNNDLTS
CCFSDAKTMYEVFQRLGAVSDNGPCLGRRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQVFVGIFAQNRPEWIIISELACYTYSMAVPLYDYLGPFAIVHVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKVEHAYEPTPDDVAISYLPPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKEKQKGIIRHDSFWDKLIFAKIQDSLGGRRVRIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTPLPGDWTSGHVGVPPLACNYVKLEDVADMMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGIDGRWLPNGTLKIIDRKNIFKLAQGEYIAPEKINIYNR
SQPVLQIFVHGESLRSSLVGVVDPDVLPSFAAKLGKSGFEELCQGVVAREAILDLQKI
GKESGLKTFEYOKAIFLHPEPFSIENGLLPTLTKAKRGELSKYFTFOIDSLYEHIOD
```

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCGCGGGCAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG
 CCGGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACCATTTGGTACGCCGCCAAT
 CCGGTATGACGACTGGAAGCCACGCCCCCTCATCAAGCCCTTTGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCGGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCTGGACA
 CTCGGCGAGCATCAGTGAAGCCAAATGAAGACCCAGAGCCAGACAAGACTATGATGAGGCC
 CTAGGCCGCTTGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGTCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGGCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGCGCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAGGAGGTCTGTCTTTCGGGGAGAAACATTTC
 TAAGTCACTTGCCTCTCTTCTGGGGGAGCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTGCGCCGCGGGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAAACAGGTCTCAATGTGGCTGTGGCTGTCAATTGAG
 GGAACCGGACCAATTACTCTACAGGATGCTGCGCTCTGCTTTACGCCACGGGGGTGTCT
 CCTCAGATTGATAACAGTTTTTCATTGACGGCTACTATGAGAACCCATGAGTGTGGTGGCAT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTGTGTGGTGT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCTGAGCCAAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCAGCACTACTGTACCCTGTGGAGACCATGCCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTCTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGTCATCATCCTGAGC
 TTTCCCGATCCTACCCTTTGGCATCGTCGGCTCAACATGAATGGCTACTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCACAGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAGAAGCTTATGAAGTGAAGTTACAGGGTGTCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTCGAATGGAGAAGATGATGACTTACCACCTGGACCCAGCTTGCCAAAGTGCCTCCA
 TATCTGGGACCTGGATGTGGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
 ACCCCAAATTTCTGGAGCCACCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
 ATGACAGCTCCTCAGGACCTGCGGGGCTGGGTACTGTGTACCCCGAGCTGGCTAGCCCT
 TCCCTCCATCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTGTTTTAACA
 TGAGACTTAATTACTAATCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTCGAGTT
 AAAAGTCTATTTATTTACTTCTTCTGTTGGAGAAGGCAGGAGATACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCTGCCCTTTGAATACCCCTCACTTTCAGGCCGTGGCTCAGAATCTA
 ACCCTATTATTGACTGTCTGAGGGCCTTGAACAACAGGCCAGCCAGTGGAGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCCTTA
 GACACTGGACAGGCCCTCCTCTCAGCCTTCTCTTTGTCCAGATTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTVIVNIKLILDTR
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REQGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDRTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRRCCKVEGYGSVCCKDPTPIEFSPDPLPDKNVLPVAVIAGN
RPNYLRLRLRSLLSAQGVSPQMITVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDOGYEHTA
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVDRGNHRLGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPKKEGAPGAPEQT

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAAGCTGGAAGGCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACTTAAAGCACCATTAAAGCCACTGGAATTTGTTGCTCTAGTGGTTGTGGGGTGAATA
 AAGGAGGGCGAAT**TGG**GATGATTTCATCTCCATTAGCCTGCTGCTCTCGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
 GTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATCTTTGAGGGAAAACACCAAGCAAGCAAGTGAACACATATGTGATTGCATCAGACAAGACGAG
 AGAAAAATCAGTTGTCCATGAACATGAGCAGAGCCACGACCACACACAGCTGCATGCCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTTCT
 ACTGACGATCCAGAAGCAGCAAGGCTAGCAATCCAAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTTCGTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTGTTGGCAATCATGCTACATAAGGCCACCAGCTGCTTTGGACTGGTTTCCCTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACCTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCAGACCCACAAGCCGATGCCACGGGAGGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCT
 GGTCTGGGTGCTCATCCCTCTCATCTGTGCTAGGACACCAGCAT**TAA**ATGTTCAAGGTCACG
 CTTGGTCCAGGGCCGTTTGGCATCCAGTGAGAAGCAGCCGCGCAGTGACAGCTACTCACTTCTCAGTC
 TTTGTCTCAGCTTGCAGATCTCATCATGTAATCTCAGAGTCCAGAGGGGAGGTGAGGTTAAACACTG
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 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAAACCTATTCTCAGGGAAGATG
 GAAATTAGTTTTAAGAAAAGAGGAGAATTCATACTCACATGAATGATGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGGTCCCACCATGTAAGACTGGTGCTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGTCAGGAAATGATAGC
 AAGACACATTGAAAGCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCCTCTGTAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCTTGTCAAAGTTCTCCTTGCAGAAAT
 ACCTGTCTCCACATTTCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCACAAGGTGCTTTTGGAAATTAAGGGATATTAATTTAAGTGATTTTTGGATGGTTAT
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 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACAGTACAGCTTT
 GGCAGACTGTGCTTCTCACAATAACCACTGTAGCAAGATGGATCATAAATGAGAAGTGTTCCTTA
 TTGATTAAAGCTTATTTGGAATCATGTCTCTTGTCTCTTCGCTCTTTCTTTGCTTTTCTCTAACTTT
 TCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAACTGTAATAATGAAGATAAATAATCTTTATTTCTTTATCCCCTT
 CAAAGAAATTAACCTTTGTGTCAATATACCATTTCAAACACATTACACTAAGGGGGAAACCAAGACTGT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACAGTTTCTATGACGCATAAGCTAGCATGCCATGT
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 GGCCACAGTGGAGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCACTGGCAACAAATGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCTTGATGGATGTGAACAGCT
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACATATATGGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTTGGTGAA
 TAACATCACCCAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAAGTTAAAGACCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGTGTTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
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 AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVKNLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLOQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEFPQPRLQAAGLPHTVEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDITINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATG CAGAAAGCCTCAGTGTGCTCTTCTGGCTGGGTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCTGGGTCCC
 TGGCATGGGGAGCCAGAGGAAAGCTGGGGCTGCTGGATGGCTCCCGATTTTTCGGGGTTGTGTGGTCTGA
 TAGATGCTCTGCGATTGTACTTTCGCCACGCCCCAGCATTACACAGTGCCTAGAGAGCCTCTGTCTCCCTACCT
 TCTTGGGCAAACTAAGCTCTTGCAGAGGATCTGGAGATTACGCCCCACCATCGCCGGCTTACCGCATCTCAGG
 TTGACCTCTTACACCACCATGACAGCGCTCAAGGCCCTCACCAGTGGCTCACTGCCTACCTTTATTGATGCTG
 GTAGTAACCTTCGCCACGCCCATAGTGGAGACAACTCTATTAAAGCAGCTCACCACTGCAGGAAGGGCTGTAG
 TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTCTTCTTCCCATCTTCA
 ATCTCAGAGACCTAGACACAGTGGACAATGGCATCTGGGAACACCTCATCCCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACCATGTGGCCACAGCATGGGCCCTCACCCACCTGAAATGGCCA
 AGAAACTTAGCCAGATGGACCAAGTATCAGGGACTTGTGGAGCTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCACAAATGGAGCCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCCTTGTGC
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 CCCGATTTCTCATACTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCTCTGCTGACTACCAAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCAGCTGA
 TTGCTGAGCTGCAGCAGTCTCTCGGGGGAGCTCGGGCCATGTGTCATCAGTCTTGGGCTCGTTTCTCTCTGGTCC
 GCATCGGGGGGATGCTGCTCTTGGCTGCTCTGCTTTATCTGCTGCTGCTGCTGCTCAGTGGAGCAATATCCC
 CAGGCTTTCATTTGCGCTCTACTCTGACACCTGTGGCTCGGGGCTGGTTGGGGCCATAGGATATGCTGGAC
 TCTCGGAACATTCTGCTGAAGCTAGACTACTGCTTTAGGGGCTGTGCTGACAGTCACTTCTCTCTCTCT
 TTCTGTGTAAGGCTTGGCTGGCTGGGGTCCAAAGAGGCCCTTGGCAACCTGTTCCTCATCTCTGGGCCGCTCC
 TGTACTCTCTGCTGTTTCGCTTGGCTGTGTTCTCTCTGATAGTTTGTGCTAGCTGAGGCCAGGCCACCCCT
 TCTTTTGGGCTCAATCACTCTGCTCTGTGGTGTGCCAGCTTCACTGGAGGGCCAGCTGCTTCCACTAAGCTAC
 TCACAATGCCCGCTCTTGACCTTCAGCCACACAAACCCCCAGGGCACAATGGTGACATATGCCCTGAGGCTG
 GAATTGGTGTGCTTTATGTACAAGGGCTCAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACCACTGTTTGGCACT
 CCTCTCCTGTGCTGAGTCTCTGTCATCCATGGTGGTGGTCTGAGCCAAAGAAATTTATGGTATGGAGCTTGTGTGG
 CGGCGTGTGGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
 CCAATGCTCTTTGTGCTGGGGACTGCCCTAATGGCATTGGGTACTGCTGCCCTACTGGGCATTTGGCGTGGGG
 CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGGCATCCATGTGCTGCTCGGGCTGTAGCAGGGC
 TGCTGCTCTAGGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGCTGGTGAAGGCTGGGGCAGGCGCTCAA
 GGACAGGACTGCTCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
 TCTACCGACACATGCAGGAGGAGTTCGGGGCCGTTAGAGAGGACCAAACTCTCAGGCTCCCTGACTGTGGCTG
 CTTATCAGTTGGGGAGTGCTACTCAGCTGCTATGCTCACAGCCCTCACCTGTTGGGCTTCCACTTCTGCTGT
 TGCATCGGAGCGCATCAGCCTTGTGTTCTGCTCTGTTTCTGAGAGCTTCTCTCTCTACATCTGCTTGTGCTG
 CTGGGATACCCGTACCCACCTGTGCTCTTTTACTGTGCCATGGCAGGCACTGCGGCTTGGGCCCTCATGGCCA
 CACAGACCTTCTACTCCACAGGCCACCAAGCTGTCTTCCAGCCATCCATTGGCATGCAGCCTCTCGTGGGATTC
 CAGAGGCTCATGGCTCTGACTTGGCTGCGCTGTTTGTAGTGGGAGCCAACACTTTGCTCCCACTCCCTCT
 TTGCACTAGTGTGCCACTGCTCTGCTCTGGCTTTCTCTGTGTGAGAGTCAAGGGCTGCGGGAAGAGACAGCAGC
 CCCCAGAAATGAAGCTGATGCCAGGTGACGCCAGGAGGAGGAGGAGGCCACTGTGGAGATGCGGCTCGGG
 ATCGGCTCAGCACTCTATGCAAGCTGCTGCAGCTGGGCCCTCAAGTACCTCTTTATCCTTGGTATTCAGATT
 TGGCCTGTGCTTGGCAGCTCCATCTTTCGAGGCATCTCATGGTCTGGAAGGTGTTGCCCTAAGTTCATAT
 TTAGGCTGTGGGCTTCATGTGAGCAGCTGGGACTTCTCTGGGCATAGCTTGGTGATGAGAGTGGATGGTG
 CTGTAGCTCTGCTGTTTGGCAGCTATTTCTGGCCAGCAGAGGTAGCTAGCTGTGATTCTGCTGCTGCTGGCT
 ACAGAGAGTGTGAGAGACAGTGTAGCTGGCTGTACAGGTACTGGATGATCTGCAGACAGGCTCAGCCATAC
 TCTTACTATCATGCAGCCAGGGGCCGTGACATCTAGGACTTCATATTTCTATAAATCAGGACCACAGTGGAGTA
 TGTNCTCTAATCTGATTGATGCTGCTGAGGACAGGGGGGCGTCTCGAAGTGGAAATAAATAGGCCCCG
 CGGTGTGACTTGCACCTAATCCAGCACTTGGGAGGCAGAGGTGGGAGATTGCTGGTCCAGGAGTTCA
 AGACCAGCCTGTGGAACATAACAAGACCCGCTCTCTACTATTTAAAAAAGTGTATAAATGATAATAT

FIGURE 60

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
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MASRFSRVVLVIDALRFDAQPPQSHVPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ
VDPPTTTMQRKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVRVFMGDDTWKDLF
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCHGKHGPHHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAELFSGGEDSQPHSSALAAQASALHLNAQ
QVSRFLHTYSAAQTQDIQAKELHQLQNLFKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFFFCPLLLTPVWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFLRLA
VFFSDSFVVAEARATPFLGSGFILLVVQLHWEGQLLPKLLTMPRLGTSATNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASVMGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLVSGASMVLV
RAVAGLAASGLALLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGVSYSAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTPPGPFTVPWQAVSAWALMATQTFYSTGHQPVPFAIHWHAAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQPPGNEADARVRPEEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGGCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTG
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGCTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACACGTGGAGTCTTCGTCCACAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAGGCTAAAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCAGCAAATTTGATTTTGATTTATGGAATGAATTTGACAAA
GATTTCTTTGTGCTGCTGAAAAAATCGTGAATTAACCTTTATCACCTCAATATCTCGGATGAT
TCTAAATTTCTCATCAGGATATGATTTACTGGGAAAAAGACGTGATGTATCCAGCCTTAA
TGATCTCTCAGCCACGGGGAACCTGAGGCCCCCTCAGAGGGAAGAGAGGTTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACATACCCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCG
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGGAGAGGGGCGGAGGAAGAGCCATCGACGACCTGTGCTGACTGGGATCCCC
AAACTGGCAGGCTGTGTATTCTTCGCTGTGCAGCTTCGACCAGGATTACAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTATGAGGGAATGGGGGT
TATATGTGCGAGATGGAAAACTGATGCCAACACTTCCTTTTGCTTTTGTTTCTGTGCAAC
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
TTGTCAAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTATAGCAGCTGTGTATTG
GTTCTGCATGTAGGTCTCTTAAACATGATGGTGGGCCCTCTGGAGTCAGGGGCTGGCCGT
TGTTCTATGCAGAGAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAAATTTATTCAGG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKEQ
CARTLKQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCPESEGDGLGEEGLLSRLYEAPADRPPEGNETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
 TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
 GATGCTGCCCCTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
 TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCAACATCACTGCGGA
 GGCTTCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTGGTGGGCGCCACGTCTCTGAGTACTGCGGAGCCCAACCAGCAGG
 TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
 TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
 TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCACCCCAAGACCCCGAC
 GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
 CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT
 TGCGGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
 AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPFYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLTAEPTQQVFGIDALTIHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRPLPGRRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTTLMLCTRSGDSHRRGFCSDSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACGGTAG
 CAGGCGCCGCGTGTCTCAAGGACTATGTACCCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCACAGGAGCTGAGCCGCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
 GGTGGCCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCAGAT**TAA**CTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCTATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGACAGGCCAGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGAGTGAAGTGTCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGTCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCC
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCTGGGACTCCCACCTTCCATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDEGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

1007567-16-04

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTCGGGCTCGGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTGTTGCATTTACTCTCATCAAACGCCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGAGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGGTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTTGGTAGC
 TGAGGCTGTCTCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCTGGGTCTCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTTCATCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCTCAA
 CCACCGCATTTGCTGCCCTCAGGCGCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTAGCTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGTTGGGAGATAAGTGGTGGCCAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCCTGAAGACT**GGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCTCGCAAAATCAGAGGC
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAAGATAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGAGGAAGTTCTGG
 AGTTCAAGTACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGCATCAGTGGGT
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTCGAGGAG
 GGGCTAGCCTGACTCCCAAGACTTAAAGACTTTCTCCCACTGCTTCTGCTGCAGCCCAAG
 CAGGAGTGTCCCCCTCCCAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTT
 TTTAAGTTGAAAACACTTTCTTTTCTTTTGTATGATGTTTTTTAACACAGTCATTAAAA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMAVNLYKERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGTGGCTGAGGGACCGAGCCGAGAGCCCCGGAGCCCCGTAAACCCGCGCGGGGAG
CGCCACAGATGC CGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCCTTGACCTTCCGGAACCAGACCATTG
ACTTCCTGAACGACAACATTGGAAGGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTAGAAAAAGTTCAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GACGAAGAAATCAGTACCACGACTGCAGTGCCTTGACCCCTGGCCCTGGCCTGGGGTGCCCTACA
CCTGCTGCATCAGGAAACAGCAGAGTGTCTCAACACCATGTGTGGCTAGAAAACTATCAGAC
AAGAGCGCTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTCTATGGACAACACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACC CGGGTGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGTACCCCAATTAGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCTCCCTTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCACCTGGGGCTGGGGAACAAGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAAACATTTCTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATAACAAGCTGGTATTTTCCGATCTTATTTCTTGCCCTTCCCCAACCAAGATTGTTTAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLIISTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILLGVVMFMVSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALTFRNQTIIDFL
NDNIRRGIEYDDLDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTYCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGAGACTCCAGCGTGCCCAGGTCCTGGCATCTGCACCTTGTGCCCTCTGA
CACCTGGGAAGATGCGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAGCCAGCCGGAGGCATCCCTGTGCTGGGAGCCTGGTGAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCAAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGGCATCTCTGCCAATCTAGTGAAAAACCAAGCTGTGGCCCGT
ATCGAGGCTTCCTTCAATGGCATGCTATGCAGACCTCTGCAGCTGGTGAAGGTGCCCAATTTC
CCTCAGCATTGACCGCTGAGAGTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCAATTC
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTACGCCTCATCGTGAGTCA
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCTGTGG
ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGTGGCCCAACTGATCGTGTGGAAGTGTTCCTCCCA
GTGAAGCCCTCCGCCCTTTGTTTACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTG
AAGGCCTTGGGATTGAGGCAGCTGAGTCTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGGCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKELTQELKDNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSIL
LPNQNGKLRSGVPVSLVKALGFEESSLTKDALVLT PASLWKPSFPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GACGGAAC**CAT**GGCAGCGCCTTGGCCGGTTTTGGTGTGTCTCTGTGACCATTGTTGGTGGCCGTG
 CTCATCGTTTGGCAGCTTCCCTCAGCCTCTGCCCAAAGAAAGGAGATGGTGTATCTGA
 AAGGTTAGTACGCTGATGGAATGAGCTAACAAAGACCTGTAAATAAGAAATGAATGGAGACA
 AGTTCCGTCGCCTTGTGAAGGCCACCGGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTCCTTTGCAAGCAAGCTGTAGGAAGATCCAGATCCTGGC
 AAATCCTGGGCATATCCAGTGCATTACCAACAGGATATTGTTTGGCAATGGTGGATTTTG
 ATGAGGCTCTGTATGTAATTCAGATGCTAAACATGAATCAGCTCCAATTTCATCAACTT
 CCTGCAAAGGGAACCCAAACCGGGGTATACATATAGTTACAGTGCAGGGTTTTCCAGT
 TGAGCAGATTGCCCGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATATTGCTGCTCCCTTATGTTGGGATTCGTTTGGCTGTTATTGGTGACGTGTGTAT
 CTTGGAAGAGCTAATAATGAAATTTCTTTAATAAACTGGATGGGCTTTTGCACTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATTGGCC
 ATAAGAATCCCCACACGGGCATGTGAATTAATTCATGGAAGCAGTCAAGCCAGTTGTGA
 GCTGAACACACATGTTCTCTGTTTATGTAGTGGATGTTACCTTAGAATGGTGCTTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAACGGAAGATAATGTGTGGCTGGTATTG
 CACTTGTGTTATATTCTTCAGTGGATGCTCTCTATTGTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGTAGATGT**TA**AAAGGTCCTCAGAGATATATAGACATGGAGTACGGAA
 ATTGAAAAACGAAATCGTGTGTGTTTGAAGAAAGAATGCAACTTGATATTTTGTATTTA
 CTCTTTTCTTCAAGTGTTTAAATAGTTAATCATTTAACCAAGAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGCAAAATCTGAGGATTTGAAATAAATATCTCTTAACCTTCTCT
 CCCAGTGAACTTTATGAACATTTAAATTTAGTACAATTAAGTATATTTAAAAAATTGAAAA
 CTACTACTTTGTTTGTAGTAGAACAGCTCAAACTACTTTAGTTAACTTGTCATCTGAT
 TTTATATTGCTTTATCCAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATACTACATAGGAATTCATCTTAGCTTCTTCACTTTTGTGTGGATGTGAT
 ACTTACGACATTTTCCCTTTGAGTAGAAGAAATATGTGTGATCTGGTCTCTGAAATG
 GAACACCATTTCTCAGAGCACACGCTCTAGGCTCAGCAGACAGTTGTTCTCTCTCTCTCT
 GCATATTTCTCATCTGCGCTCCAGCCTGAGCTGATAGTGAGAGCTGTCTTCAAAAAAGTA
 TCTCTAAATACAGGATATAAATTCCTGCTGTAGTATGGTGTAACTACCTTGTAATTAGAAA
 GATTTCAGATTCATTCCATCTCTTAGTTTTCTTTAAGGTGACCACCTCTGFGATAAAAAATA
 TAGCTTAGTGTCAAAATCAGTGTAACTTATACATGGCCTAAAAATGTTCTACAAATAGAGT
 TTGTCACTTATTCCTATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CAGGCGCAGTGACTTACCGCTGTAACTCTCAGCACTTTGGGAGAGCCAGGCGAGCATCAC
 GAGGTGAGAGATCTCGAGACCTCTGCGCAACATGTTGAACCCCGTCTCTACTAAAAAAT
 AAAAAATTAGCTGGGTGTGGTGGCAGGAGCTGTAAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAACTCACTGAACTCAGGAGATGGAGTTTTCAGTAGGCCGAGATCAGCCCACTGCATCC
 AGCCTGGCAACGAGCGAGATCCATCTCAAAAGAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCGGCTGGCCCCGGCGGAGGCTCTCAGAACCGGTACCGGCC**ATG**CTA
 CTGCTGTGGGTGTCGTGGTTCGCGAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCGTGAGCGACTCCTTCGATG
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAACCTTCCTTTTATCAACTTTATGAAG
 ACACGTGGGACTTCCTTTCTGAATGCCATACACAACTCTCCAATTTGGTTGCCCATCACGGCGC
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAAATAATTTAAGGGCTCAG
 ATCCAAATTTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAACTGGACTATACCTCAGGACATCACTCCAATAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA
 CTAAAGTCAGAGTGATGGAAGGGATTGCGAGAATACAGACAAAGCAGTAACCTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAATTTACCACACCC
 TTACCCCTTACCATCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAATCCCAAAGTGGTCACCTTTGTCCAGAAATG
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AAATTAATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTTTGTCAATACTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCGCGGCTACAAGTCAAAATG
 TGGTTTCTCTGTGGATATTTACCCTACCATGCTTGATATGCTGGAATTCCTCTGCCCTCAG
 AACCTGAGTGGATACCTTTGTTGCCGTATCATCAGAAACATTTAAGAATGAACATAAAGT
 CAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTCCGATGGTGCATCAATATG
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAATTTCC
 AGAAATTACTTTATCTTTGGATCAGAAGCTTCATCCATTATAAACTACCCCTTAAGTTTCTG
 CTCTGTCCACCAGTATAATAAAGAGCAGTTTTATCAAGTGGAAACAAAGTATAGGACAGAAAT
 TATTCAAACGTTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAATGCAATTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTT**TGA**CAAAAAA
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAAGTCATAATTATGATTTT
 AAATGAAACAGTTTAAATAATTACCAAGTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAGGTCAGAGATGAGACCATCCTGGC
 CAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGCGCGGTGGTGACA
 CCTATAGTCTCAGCTCTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCACTGAGCTGAGATTGCCCCACTGTACTCCAGCTGGCAACAGAGTGAGACTGTGTCGC
 AAAAAAATAAAAAATAAATAATAAATACCAATTTTTCATTATTTGTAAAGTGTAGTG
 TATTTAAGATAAAATGCCAATGATTATAAAAACACATATTTTCAAAATGTTTATATTTA
 GGCCTTTGTACAATTTCTAACAAATTTAGTGGAGATATCAAAGGATTGAAGCAAATACTGTA
 ACAGTTATGTTCTTTAAATTAATAGAGAATATAAAATATGTAAATATGTATCATAAAAAT
 AGTTGTATGTGAGCATTTGATGGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

100% 75/249
 100% 75/249
 100% 75/249

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQSVNVVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFP EITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCCAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGAGGGCTCCTGGGATTCATTCTGTGCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTCCCTGTTCTCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTG**TGA**AAGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCCCTCAACTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTGTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCCAGGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCT**TG**AGAAGACATAGAAAGAAAATCAACTTTCCTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTCTACGACCCCCGTCAGCACTGTT
GCTATGATGATGCCGTGCTGCCCTTGGCCAGGACCCAGACGTGTGGAACATGCACCTTCAGA
GTC'TGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGGCA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTACGTAAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTCGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGA
TCTGGGATGCTGAGTGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCCACCTGCGAGCTGCCCTGAGGAGGCCACAGGTCCCTTCTAG
AAT'TCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACTCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCTT
TCTGTGAGATTTTCCATCATCTCAAGTCTCTTCTATCCAGGAGCAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCI VAVFAIFCISRL LCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

1003527.2401

GGGGGCGGGTGCCTGGAGCACGCGCTGGGGCGCCCCGACGCTACTCGCTCGCACTACG
TCGCGGGAGGCTTCCCCGCGCCGCGCTCCCGCCGCTCCCCGGCACCAGAAGTTCCTCT
GCGCGTCCGACGGCGACATGGGCGTCCCACGGCCCTGGAGCCGCGAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTCGC
CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGCGAAGCTCACCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAGGGGACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGCGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCTCTCTCCAGGATAGTGAAACATCAGGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCTTGGTCTACAAGCAAGGACAGGCAC
CTCCAAACGCGCTGCCAGGAGCTGTCGGATGGACGACCAATTCAGGGATTGAAACCC
CCGGCTTTGAAGCTCTCACCAGCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTTCGGAGCCAGCAC
CCCCCTGTCTCTCCAGGCCCCGAGACGTCTTCTTCCCATCCTGGACCCTGTCCCTGACT
CTCCAAACTTTGAGGTCATCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGCCCTCGGCCCTGGTTT
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCGTTCAGGATTTTGGGGTGTGAG
ATTCTCCCTAGAGACCTGAAATTACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCAGCCCTTACGACGCTCTCGTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCTCCAGGCACAGACAGGGGACGGTG
GAGAGACTTCTCCCCGTGGCCGCCCTTGGCTCCCCCGTTTGGCCGAGGCTGCTCTTCTGTC
AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCATGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCACTGGAGATGGTGTCTGAGGGAGGTGGTGGGCGCTTCTGGGAAGGTGA
TGTGAGAGGGGACACTGCCCCCCGCCCTCCCCATCCCCACTCCCCACTCTGAGCGGGGC
ATTGCAAGGTTGCCACCAATGCTTGTCTACCCCTGGGACACTCTGAGTATGAAGCGGGAT
GCTATTAAAAACTACATGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALAASLGPVAAFVKVATPYSLYVCEGQNVTLTCRLLGPVVK
GHDVTFYKTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTCTGCCCTCC
 TTTCTGCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
 CTCGCTCCCGGACCAGCGGCTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGTCCTC
 TCCTCCTTGTCTGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTAAGCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACCCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCTCC
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCGTCCTTCGGCCCCCTTGCCTTG
 CATCTATGCACCTGTGAGGATGGCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT
 ACCCTGCCGTCAACCCGAGAAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTCGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGTCACTGGAACGTCTTCTAGCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSGCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGGFTPAPTGLSAPLSFIPRHRFPKGAGSTTVKIVLKEKH
KKACVHGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL
KDEETEAQRGEVFGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPFG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGAGCTCCC
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCTTGCGGAAATGCTGATCTCAGT
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCGGGAG
 AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
 CGTGCCCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGCGGCGCCAGCGGGAGGTCACCGT
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGCTTGGGCGCAGGAATCCGAGGCAGCC
 TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
 TCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCAAACCCTGGACTGACTGCTTTAAGGT
 CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAA
 TCATGTTCTCCAA
 AAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

1007527-10100

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLLILFLLSWSGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGTYTISQVRSMKILKRFGGPPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWPVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPFAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ
QWDTPCPRENAEAAFVICGLTYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPFRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGAAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCTCCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGTACTCTGTCTCAGTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTCTCCAATTCAGTGAAAAATCCAGGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACAGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAACGTGAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGAGCTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAAGTCTCCTCACAGGCAACCACGCCCTTCTCCCCAGG
 GTGAAATGTAGGATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCTGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATCCCATCTCACAGGCTGTGGTGATAGTAAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCAATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRRFRGQFSS
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAE LDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATT PFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCCGGTGGCGGTGGCGGGCGGCGGTGCGGAGGCTTCCCTGGTCGGATTGCA
 ACGAGGAGGAAGATGACTGACCAACCGACTGGCTGAATGAATGATGGCGGAGCCGAGCGCGC
 C**ATG**AGGAGGCTTGCCGAGCCTGGCGGGCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGCAGGTG
 GACGCGTCGCCGGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC
 TCCCACGGGCCAGGCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGGTG
 CGACTTCTCCAGCCAGTCCCCGAGACCCACCCCTTTTGGGCGACTGCTGGACCTCTTCC
 ACCACCTTTCAGGCGCGCTCGGCCCCCTCGCCGACCACCCCTCCGCGGCGGAACGCACCTT
 GACCACCTCTCAGGCGCGCAGACACCGCGCCGACCACCCCTTCGACGACCACTGGCCCCG
 CGCCGACACCCCTGTAGCGACCCGTACCGGCGGCCACGACTCCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCCACTGCCACCGAGGCCCCCTC
 TTCGCCTCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGAAGTGAAGTTTATT
 TTATTTTAGCAAGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAG
 GAGGATGAGGGTCATAGATTACAAAAATATTTATATACTTTTATCTCTTATTTATATGT
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTCTTCTCAAAGCAGTAG
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAAATTTTATGGGAAAAAATTATTGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTTCAAGCATGAAACCTGCTAGGAGGTTTGAAGATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAAGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAAATCTACATTTGTTTCTTTGGACATCTAAAGCTTAACGTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGACCAAAAG
 TAGATTAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGA
 ATAATGTACTGTTATCTAAGCATTGCGTTGACTGCACCTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGTTTATCTCAGTGTAACCTGGGTATAACCCAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGCAAGTAATTTCTTTCACTGAGCTTGTCTCTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATAAAAAATGCCTAGCACATGCTCACTCAATAAA
 TTCTGGTTTGTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAATGTTTAAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATTTTAAATGCTTTA
 TAAATGATATTATACCTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAACAAATAGCTGGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAAGTGAATCGCGCCACT
 GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSIPLSLGGLALLCCAAAAA AVASAASAGNV TGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETT PLWATAGPSSTTFQAPLGPSP TTPPAAERTS
TTSQAPTRPAPTTLS TTTGPAPTTPVATTVPAPTTPTPTDLPSSSNSSVLTPPPATEAPS
SPPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLYNTSGLCQPCDCSP
HGALSIPCNR

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

TGC GCG CAG TGT AGA CCT GGG AGG CAT GCG CGC CTG CTG TGG CTG CTT TCT GGC TTT GG
 TCT CGG TCCC AGG CCC AGG CCG TGT GGT TGG GAA GACT GG ACC CTG AGC AGC TCT TGGG
 CCT GGT ACG TGT TGC GGT GGC CT CCC GGG AAA AGG CTT TGC ATG GAG AAG GAC ATG AA
 GA ACG TCG TGG GGG TGG TGG TGA CCT CACT CCA GAA AAA CACT GCG GAC GCT GT CCT CTC
 AGC ACG GGT GGG AGG GTGT GAC CAG AGT GTC ATG GAC CTG ATA AAG CGA AA ACT CCG GAT GG
 GT GTT TGA AAT CCT CAAT AGG CGT GCT GGA GCT CTG GGT GCT GGC CCA CAA CTT CAG AGA
 CTAT GCC ATCAT CTT CACT CAG CTGG AGT TCG GGG ACAG GCC CTT CAA CAC CGT GG AGC TGT
 ACAG TCT GAC GGA GAC AGC CAG CAG GAG GCC ATG GGG CTT CTT ACCA AGT GG AGC AGG AGC
 CTGG GCTT CCT GT CAC AGT TAG CAG GCC CAG CTG CAGA AGG ACCT CAC CTG TGT CACA AGT
 CCT TCT GT GAG TGT GCG TCCC AGT AGG GAT GGC GCC CAC AGG GTCT GT GAC CTG GCG CA
 GTG TCC ACC CACT CGCT CAG CGG CTCC GGG GCC CAG CAC CAG CTG AGA ATA AAG CG ATTC
 CAC AGA

FIGURE 96

MGGLLLAAFLALVSVPRQAQVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAII FTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

10017527.12302

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCCTGGATTTACCCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGCCAAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCCTGGAGTCCGGCTGCCCCAGAACTCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAACCGCTGTCAGGGGTTAGCCT
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATGA**G**AAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDREHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNGSSSLPPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDGTGIEDANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGEQELQYA
SLSFQMPKPDWSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATG**AAGACCCTGTTCCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCACCCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVS PVKV TALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCGCGAGATGCAGAGGTTGAGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
GGCGACGTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGTGTTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGTTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTGTGATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRIQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDSSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCGTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGCAGCCGGA
CACAAATGAAGGCCACCCAAATGGTTTGTTCTTGGTGTGGGCAAGTCATAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
GAAC**TAG**CATATTTGTATTCTACTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTGCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 1

[illegible]

Figure 1

[illegible][illegible]

Figure 1

Figure 1

[illegible][illegible]

Figure 1

Figure 1

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACAAAACCTTCCTGTGCTAAGTGCCCCCAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

1007527-249

FIGURE 106

MQGP L L L P G L C F L L S L F G A V T Q K T K T S C A K C P P N A S C V N N T H C T C N H G Y T S G S G Q K L F T F P L
E T C N A R H G G S R L

Signal peptide:

amino acids 1-18

106/249 106/249

FIGURE 107

CAAGCAGGTCATCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCAGACTTTGGAAGTGACCCACCATGG
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGCTTATTGACCACAGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCC GGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCTGCCCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACC AACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGTCTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTGCAAGTATGTGGAAGTGGATCCGGATGATCATGAGGAACAACTGAC
 CTGTTTCTCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTTCTTGGAACCT
 AATATCTCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTTCTTGGAACCT
 TAACTCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGFGCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

108/249

FIGURE 109

CGCGGCCACACGCGAGCTAGCCGCGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGCGTTTCGGCTTGCTCAAAGCCCGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAAACCTTCCAGAAAA
GCTCAGACCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGCGAGATTGAC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGCTGCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
GGACCCCGCCTGGACTCCCAGCCTTCCCACCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTTTGTGTTT
TCATCAATGTCTTTGTAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGAATCC
TGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGAGGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGAGTAGGGACAAGG
CTGCAAGGGCCTCTTCGGGTTTCCTTGACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTCAAGAAGG
TACCAGAAGGAACCTCCAGTCCTGCTCTCTGCGCACACCTGTGCAGGCAGCTGAGAGCGAG
CGTGCAAGCTACTGCTTCTACTGGGGCAGCAGAGGGCTTCGGAGGACAGAAGTGAGGGCTG
GGGTTTGGGGGGAAGGTCCTTCTGAGTGCTGTTCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAAATGCTCAGCGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAfKEKYMEDLN
NEGEIDLMSLKRMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGGCCCTGCACACCA~~ATG~~CCCCCGGGTGGGACAGGGGTGCGCGCGCCGTGCGCGCC
 CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCCTGAGTGGGCTCCAGCCGTGCGCCTGGCC
 CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCTCCGCGCGGTTC
 CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
 ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGACTTGGGAAGACAACAGGT
 CAGCGTCATCGAGAGAGGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCGCAAGCTCACCAGACTA
 GATTTGAGTGA~~AA~~ACCAGATCCAGGGGATCCCAGGAAGCGTTCCGCGGCATCACCAGATGT
 GAAGAACCTGCAACTGGACAACACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
 TGC~~CG~~GATTTGGAGTCTTACCTTCAACAACAACACATCAGTCGCATCTTGGTCACCAAGC
 TTCAACCACATGGCGAAGATCCGAACCTCTGCGCCTCCACTCCAACACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTCACTCT
 GCATGGCTCCTGTGCAATTTGAGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGATACGTG
 TGCCAGCCCCCACTCGGAGCCCCATCTGCAATGCCAATCCATCTCTGCCCCCTGCCC
 CTCGACGTGCAGCAATAACATCGTGAGCTGTCGAGGA~~AA~~GGGCTTGATGGAGATTCCTGGCA
 ACTTGGCGGAGGGCATCGTCGAATAACGCTTAGAACGAACTCCATCAAAGCCATCCCTGCA
 GGAGCCTTCCACCGATCAGAA~~AA~~CTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCAGATGCTTCCAGGGCTTGAATCACTACATCCGCTGGTCCGTGATGGGAACA
 AGATCACCAGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGTGTCTCTCTC
 AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTTCAGGACCTGCAGAACCTCAACT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTCGAGT
 CCATCCAGACACTCCACTTAGCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGCCGCTGCAGCAAGCCGCGCGG
 ACTCGCCAAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCAGCGAGTGTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
 TGTGAGGGCAGGATTTGGAGTGTCTCAACCAGAAGCTGGTCCGCAATCCCAAGCCACCTCCC
 TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTCTTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACACGCT
 GGAGACCGTGCCAGCGGGCGGCTGTTCGTGGCCTCAGTGGCCTCAAACCTTGTATGCTGAGGA
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCGCGCCTGAGTTGCGTGAGCTGGTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTCCCTC
 AAGGAGATTCCATCCAGGATGTGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT
 CGAGCAACAAGGGGCTCCGCGCCCTCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGA~~AA~~ACCACTAAACGCCGTGCCAGAGAGCTGTCCGCCCCCGACACCTGACGCT
 TATTGACCTGAGCAACAACGATCAGCATGCTGACCAATTACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCTTCAAC
 GGGCTGCGGTCCCTGCGAGTGTAAACCTTCCATGGCAATGACATTTCCAGCGTTCTTGAAGG
 CTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCATCCACTGTG
 ACTGAGTCTTCCGTGGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGACCTGGCATCGCC
 CGCTGCGATAGCCCTGAGCCATGGCTGACAGGCTCTGCTCACCAACCCCAACCCGCTT
 CCAGTCAAAAGGGCGAGTGGACATCAACATTTGGGCCAAATGCAATGCCTGCCTCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACCTGTGCCCATCAACACCTGCATCCAGAACCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAGGATGGGTTCAGCTGCTCCTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCAGATGACTGTGAGGACACAGCTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACTACGTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAAGCTG
 AGGCCAAGTGATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG
 AACACCCCCACCCATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCGAAAC
 GGGGCCCAGTGATCGTGGTGCAGCAGGAGCCCACTGCCGCTGCCACCAGGCTTCGCCCG
 CCCAGATGCGAGAAGCTCATCTGTCAACTTCGTGGGCAAAAGACTCCTACGTGGAAGTGG
 CCTCCGCCAAGTCCGACCCAGGCCAACATCTCCTGCGAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTCCCTCCAAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG
 GACAAAGGAATCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGGCCAGGGCACGG
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACAGAGCTGCAG
 GACTTCAAGGCCCTCCACCACAGTCCCTGGGGTGTCAACAGGCTGCAAGTCTGCACCGT
 GTGCAAGCAGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCACTCTGCGACCAAGGAGGCCGGGACCCTGCCTCGGCCACAGATGCCAC
 CATGGAATATGTGTGGCAACTGGGACCTCATAATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAAGAGAATCCGTGCCGTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGCT
 GTGGGCCCAAGTGCTGCCAGCCCAACCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGACG
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
 CTAAAGCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGTATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
 AGAGAATATTAGTATATTGTAAATAAACAATAAATAAGAACTTAAAAAAAAAAAAAAAAA
 AAAAA

FIGURE 112

MAPGWAGVGAARARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNNHLYCDCHLAWLSDWLRQRRTVQGQETLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAI PAGAFTQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIISKGLFAPLQSIQTLHL
 AQNPFCVDCCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFS
 SECMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISC
 VNDTFAGLSSVRLLSLYDNRITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKR
 IVSGNPRCQKPFELKEIPIDQVAIQDFTCDGNEESSQLSPRCPEQCTCMETVVRCSNKG
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTLDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLTLLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIP
 DKGFSCECVPGYSGKLCTDNDDCVAHKCRHGAQCVDITINGYTCTCPQGFSGPFCEHPPMV
 LLQTSPCDQYECQNGAQCIIVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDLSPPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-1049-1050-1051-1052-1053-1054-1055-1056-1057-1058-1059-1060-1061-1062-1063-1064-1065-1066-1067-1068-1069-1070-1071-1072-1073-1074-1075-1076-1077-1078-1079-1080-1081-1082-1083-1084-1085-1086-1087-1088-1089-1090-1091-1092-1093-1094-1095-1096-1097-1098-1099-1100-1101-1102-1103-1104-1105-1106-1107-1108-1109-1110-1111-1112-1113-1114-1115-1116-1117-1118-1119-1120-1121-1122-1123-1124-1125-1126-1127-1128-1129-1130-1131-1132-1133-1134-1135-1136-1137-1138-1139-1140-1141-1142-1143-1144-1145-1146-1147-1148-1149-1150-1151-1152-1153-1154-1155-1156-1157-1158-1159-1160-1161-1162-1163-1164-1165-1166-1167-1168-1169-1170-1171-1172-1173-1174-1175-1176-1177-1178-1179-1180-1181-1182-1183-1184-1185-1186-1187-1188-1189-1190-1191-1192-1193-1194-1195-1196-1197-1198-1199-1200-1201-1202-1203-1204-1205-1206-1207-1208-1209-1210-1211-1212-1213-1214-1215-1216-1217-1218-1219-1220-1221-1222-1223-1224-1225-1226-1227-1228-1229-1230-1231-1232-1233-1234-1235-1236-1237-1238-1239-1240-1241-1242-1243-1244-1245-1246-1247-1248-1249-1250-1251-1252-1253-1254-1255-1256-1257-1258-1259-1260-1261-1262-1263-1264-1265-1266-1267-1268-1269-1270-1271-1272-1273-1274-1275-1276-1277-1278-1279-1280-1281-1282-1283-1284-1285-1286-1287-1288-1289-1290-1291-1292-1293-1294-1295-1296-1297-1298-1299-1300-1301-1302-1303-1304-1305-1306-1307-1308-1309-1310-1311-1312-1313-1314-1315-1316-1317-1318-1319-1320-1321-1322-1323-1324-1325-1326-1327-1328-1329-1330-1331-1332-1333-1334-1335-1336-1337-1338-1339-1340-1341-1342-1343-1344-1345-1346-1347-1348-1349-1350-1351-1352-1353-1354-1355-1356-1357-1358-1359-1360-1361-1362-1363-1364-1365-1366-1367-1368-1369-1370-1371-1372-1373-1374-1375-1376-1377-1378-1379-1380-1381-1382-1383-1384-1385-1386-1387-1388-1389-1390-1391-1392-1393-1394-1395-1396-1397-1398-1399-1400-1401-1402-1403-1404-1405-1406-1407-1408-1409-1410-1411-1412-1413-1414-1415-1416-1417-1418-1419-1420-1421-1422-1423-1424-1425-1426-1427-1428-1429-1430-1431-1432-1433-1434-1435-1436-1437-1438-1439-1440-1441-1442-1443-1444-1445-1446-1447-1448-1449-1450-1451-1452-1453-1454-1455-1456-1457-1458-1459-1460-1461-1462-1463-1464-1465-1466-1467-1468-1469-1470-1471-1472-1473-1474-1475-1476-1477-1478-1479-1480-1481-1482-1483-1484-1485-1486-1487-1488-1489-1490-1491-1492-1493-1494-1495-1496-1497-1498-1499-1500-1501-1502-1503-1504-1505-1506-1507-1508-1509-1510-1511-1512-1513-1514-1515-1516-1517-1518-1519-1520-1521-1522-1523-1524-1525-1526-1527-1528-1529-1530-1531-1532-1533-1534-1535-1536-1537-1538-1539-1540-1541-1542-1543-1544-1545-1546-1547-1548-1549-1550-1551-1552-1553-1554-1555-1556-1557-1558-1559-1560-1561-1562-1563-1564-1565-1566-1567-1568-1569-1570-1571-1572-1573-1574-1575-1576-1577-1578-1579-1580-1581-1582-1583-1584-1585-1586-1587-1588-1589-1590-1591-1592-1593-1594-1595-1596-1597-1598-1599-1600-1601-1602-1603-1604-1605-1606-1607-1608-1609-1610-1611-1612-1613-1614-1615-1616-1617-1618-1619-1620-1621-1622-1623-1624-1625-1626-1627-1628-1629-1630-1631-1632-1633-1634-1635-1636-1637-1638-1639-1640-1641-1642-1643-1644-1645-1646-1647-1648-1649-1650-1651-1652-1653-1654-1655-1656-1657-1658-1659-1660-1661-1662-1663-1664-1665-1666-1667-1668-1669-1670-1671-1672-1673-1674-1675-1676-1677-1678-1679-1680-1681-1682-1683-1684-1685-1686-1687-1688-1689-1690-1691-1692-1693-1694-1695-1696-1697-1698-1699-1700-1701-1702-1703-1704-1705-1706-1707-1708-1709-1710-1711-1712-1713-1714-1715-1716-1717-1718-1719-1720-1721-1722-1723-1724-1725-1726-1727-1728-1729-1730-1731-1732-1733-1734-1735-1736-1737-1738-1739-1740-1741-1742-1743-1744-1745-1746-1747-1748-1749-1750-1751-1752-1753-1754-1755-1756-1757-1758-1759-1760-1761-1762-1763-1764-1765-1766-1767-1768-1769-1770-1771-1772-1773-1774-1775-1776-1777-1778-1779-1780-1781-1782-1783-1784-1785-1786-1787-1788-1789-1790-1791-1792-1793-1794-1795-1796-1797-1798-1799-1800-1801-1802-1803-1804-1805-1806-1807-1808-1809-1810-1811-1812-1813-1814-1815-1816-1817-1818-1819-1820-1821-1822-1823-1824-1825-1826-1827-1828-1829-1830-1831-1832-1833-1834-1835-1836-1837-1838-1839-1840-1841-1842-1843-1844-1845-1846-1847-1848-1849-1850-1851-1852-1853-1854-1855-1856-1857-1858-1859-1860-1861-1862-1863-1864-1865-1866-1867-1868-1869-1870-1871-1872-1873-1874-1875-1876-1877-1878-1879-1880-1881-1882-1883-1884-1885-1886-1887-1888-1889-1890-1891-1892-1893-1894-1895-1896-1897-1898-1899-1900-1901-1902-1903-1904-1905-1906-1907-1908-1909-1910-1911-1912-1913-1914-1915-1916-1917-1918-1919-1920-1921-1922-1923-1924-1925-1926-1927-1928-1929-1930-1931-1932-1933-1934-1935-1936-1937-1938-1939-1940-1941-1942-1943-1944-1945-1946-1947-1948-1949-1950-1951-1952-1953-1954-1955-1956-1957-1958-1959-1960-1961-1962-1963-1964-1965-1966-1967-1968-1969-1970-1971-1972-1973-1974-1975-1976-1977-1978-1979-1980-1981-1982-1983-1984-1985-1986-1987-1988-1989-1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2536-2537-2538-2539-2540-2541-2542-2543-2544-2545-2546-2547-2548-2549-2550-2551-2552-2553-2554-2555-2556-2557-2558-2559-2560-2561-2562-2563-2564-2565-2566-2567-2568-2569-2570-2571-2572-2573-2574-2575-2576-2577-2578-2579-2580-2581-2582-2583-2584-2585-2586-2587-2588-2589-2590-2591-2592-2593-2594-2595-2596-2597-2598-2599-2600-2601-2602-2603-2604-2605-2606-2607-2608-2609-2610-2611-2612-2613-2614-2615-2616-2617-2618-2619-2620-2621-2622-2623-2624-2625-2626-2627-2628-2629-2630-2631-2632-2633-2634-2635-2636-2637-2638-2639-2640-2641-2642-2643-2644-2645-2646-2647-2648-2649-2650-2651-2652-2653-2654-2655-2656-2657-2658-2659-2660-2661-2662-2663-2664-2665-2666-2667-2668-2669-2670-2671-2672-2673-2674-2675-2676-2677-2678-2679-2680-2681-2682-2683-2684-2685-2686-2687-2688-2689-2690-2691-2692-2693-2694-2695-2696-2697-2698-2699-2700-2701-2702-2703-2704-2705-2706-2707-2708-2709-2710-2711-2712-2713-2714-2715-2716-2717-2718-2719-2720-2721-2722-2723-2724-2725-2726-2727-2728-2729-2730-2731-2732-2733-2734-2735-2736-2737-2738-2739-2740-2741-2742-2743-2744-2745-2746-2747-2748-2749-2750-2751-2752-2753-2754-2755-2756-2757-2758-2759-2760-2761-2762-2763-2764-2765-2766-2767-2768-2769-2770-2771-2772-2773-2774-2775-2776-2777-2778-2779-2780-2781-2782-2783-2784-2785-2786-2787-2788-2789-2790-2791-2792-2793-2794-2795-2796-2797-2798-2799-2800-2801-2802-2803-2804-2805-2806-2807-2808-2809-2810-2811-2812-2813-2814-2815-2816-2817-2818-2819-2820-2821-2822-2823-2824-2825-2826-2827-2828-2829-2830-2831-2832-2833-2834-2835-2836-2837-2838-2839-2840-2841-2842-2843-2844-2845-2846-2847-2848-2849-2850-2851-2852-2853-2854-2855-2856-2857-2858-2859-2860-2861-2862-2863-2864-2865-2866-2867-2868-2869-2870-2871-2872-2873-2874-2875-2876-2877-2878-2879-2880-2881-2882-2883-2884-2885-2886-2887-2888-2889-2890-2891-2892-2893-2894-2895-2896-2897-2898-2899-2900-2901-2902-2903-2904-2905-2906-2907-2908-2909-2910-2911-2912-2913-2914-2915-2916-2917-2918-2919-2920-2921-2922-2923-2924-2925-2926-2927-2928-2929-2930-2931-2932-2933-2934-2935-2936-2937-2938-2939-2940-2941-2942-2943-2944-2945-2946-2947-2948-2949-2950-2951-2952-2953-2954-2955-2956-2957-2958-2959-2960-2961-2962-2963-2964-2965-2966-2967-2968-2969-2970-2971-2972-2973-2974-2975-2976-2977-2978-2979-2980-2981-2982-2983-2984-2985-2986-2987-2988-2989-2990-2991-2992-2993-2994-2995-2996-2997-2998-2999-3000-3001-3002-3003-3004-3005-3006-3007-3008-3009-3010-3011-3012-3013-3014-3015-3016-3017-3018-3019-3020-3021-3022-3023-3024-3025-3026-3027-3028-3029-3030-3031-3032-3033-3034-3035-3036-3037-3038-3039-3040-3041-3042-3043-3044-3045-3046-3047-3048-3049-3050-3051-3052-3053-3054-3055-3056-3057-3058-3059-3060-3061-3062-3063-3064-3065-3066-3067-3068-3069-3070-3071-3072-3073-3074-3075-3076-3077-3078-3079-3080-3081-3082-3083-3084-3085-3086-3087-3088-3089-3090-3091-3092-3093-3094-3095-3096-3097-3098-3099-3100-3101-3102-3103-3104-3105-3106-3107-3108-3109-3110-3111-3112-3113-3114-3115-3116-3117-3118-3119-3120-3121-3122-3123-3124-3125-3126-3127-3128-3129-3130-3131-3132-3133-3134-3135-3136-3137-3138-3139-3140-3141-3142-3143-3144-3145-3146-3147-3148-3149-3150-3151-3152-3153-3154-3155-3156-3157-3158-3159-3160-3161-3162-3163-3164-3165-3166-3167-3168-3169-3170-3171-3172-3173-3174-3175-3176-3177-3178-3179-3180-3181-3182-3183-3184-3185-3186-3187-3188-3189-3190-3191-3192-3193-3194-3195-3196-3197-3198-3199-3200-3201-3202-3203-3204-3205-3206-3207-3208-3209-3210-3211-3212-3213-3214-3215-3216-3217-3218-3219-3220-3221-3222-3223-3224-3225-3226-3227-3228-3229-3230-3231-3232-3233-3234-3235-3236-3237-3238-3239-3240-3241-3242-3243-3244-32

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCCTATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA AAAAAGGCTGTGAGGTTTCCCTAAACTGGAACCTGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCCTGTGTCATCTTGTCCTCGTTTCCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

115/249 115/249

FIGURE 115

CAGGCCATTTCGACATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCCCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCC
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAAGTGTTC
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTTACAGCTGCTGTTTTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCCTGATGTCTCTATCCATCTCTAAATGTCAACCAG
CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTTGGAGGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGGCAGGTGG
TTATGACGAGAGAGTGCTGTGGAAGATTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGCACTTTGGCCAGTGTGACTTCTCTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
CTCCTCCACAGCTGCAGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
ATAGAAAAGTTCATCCGTGAACCTTCCCTAAAAGCCACCATGGGCTTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTATGTCATTTTTATGGATTGTAGACC
CAGTTTTGAAACCAAAAAGAAACCTAGAACTCTAATGCAGAAGAGATCTTTTAAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGCCACTTTTCAGAAA
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAATGTGGTG
TCATTCCATGTTTACGAGAGTATTTTAATATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATACTGTGCCCTAATTGGTTTTTCATAGTTTAAGTGTGATCATTATCAA
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCGCCAGATCAAT
CCACCGAAGTGTCTCATGTCATCTGTAGGGAATTTTTGTTGTCCGTCTTTGGCTGGATC
CATAGGAGAGATGCTCTGTATTTTTTTAAAGATAATTTGTATTTTTGCACACTGAGATATAA
TAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGKEFKLFTLVSAIPVFRRLARRRKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAACTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGCCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAACACATGAGGAAAAAATGTATGAAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTGGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT
 CCTAGAGAGACCTCTGCTTTATGCCCTTGGTGTGTAATCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGTATCCAGATCGGTTTGATGATGAATTAGTAATGAAACTTTTTCTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAAACACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTGTAC
 TTAA

10075372500

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEVQKKLYEINQVF
GNGPVTPEKIEQLRYCQHVLCEVVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLVYALGVVL
QDPNTWPSPHKFDPDFRDELMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSREAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

10017527.121301

FIGURE 119

CTAGATTTGTCGGCTTGC GGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTG TCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTCACCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCAACCTGGGCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCTTCT**TGAT**TACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTGGAATAATTACGCTTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAAGCTTATATACAGTTTATAGGGACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPITFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCACACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAATTACAGGGTGC
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCC**TGA**GGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAACCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTEGAHSGHLWNP
MSIGISFMGNMMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

123/249

FIGURE 123

CTGGGACCCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
 GACTCGTGCTGCTTCTGTTCTCGTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAAATTCACCTCT
 CCTAGGGCTGTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGCTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCAATTCCAACAATGCCACAGGCCAGGGAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAATCTTCAACTGCCGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGACCTC
 GCTTTCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGTGTGCCAGATTACAACTACCATAGTGATACCCCCCTACTACCCATC
 TGGGTGACCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCAGGAGCACTGGAGGAGAGTGGGCT
 CTCTGTGCAGCCTCAGGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTGTGCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC
 CGGATCTGGATGGCCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGTGGGGGGAGGGAGGGAAGCTTTGT
 GAAACCGTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDFAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAA
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACCGGGCGAGCACAGCGCCAGCC
 GGGTGC GGCTGCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCGTCTGGGACAGAACGACACGGAGCC
 CATCGTGTGAGGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCA
 GAAAAGGAATTTACAGTTTCAGTTTTCACGTGATTAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGTATGTTAAATGGAAAACAGTAATATCTGCCCTTTCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTTGAATTAGTTTGTGTTGGTCTGTAA
 AAAACTTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAATCTGACAAGGAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAATGATTGATAATAACCACTTTTATTAATAACCTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACGTGGTGGTGGGATGCTGTTGTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGGTTTTGCCTTAACCTCTTTAAATGT
 ATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGAATAT
 CTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAGA
 TTAATATATGTTAAAAAA

FIGURE 126

MGSGRRALS AVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIIYSFSF
HVIKVIQSQTIQVNLMLNGKPFVISAFAGDKDVTREATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

1007527.127

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCTTTGTGAATACCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTGATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFEMARVIIDN
KDGPTQKYLILIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LKLCLLCQDKN
FLLYNQRSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACGACGCCGCCACACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTCTGGGCTTGCCCTTCT
 TGGTGCCTTTGGTGGCCCTCGGTGCGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGCTCTCGCAGAAGAGCGCCG
 AGTTTGTAGCGCAGCTTACGTGGACAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACACTTCTGTGACCC
 CGAACAGGACGAGGGCGTGGTGTCTGTGAACGCTCCTGAACAGCAGAGGGGGGCGCGTGTCTGTTTGTGG
 TCCGCGAAGAGGAGCTGTGGTGTCTTCCAGGTGCCCTTAATCTGCGAGGGATGTTTTCAGCGCAAGTCACTCT
 ACCAAAAGTTGGAACGACACCTGTGTGAGCCGCCACCAAGATGAGTCGGAGATTTCAGTTCTTCTACGTGGATG
 TGTCCACCCCTGTCAACAGTCAACACACATACAGCTCCGGGTGACCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTTCACTTCAATACCACAGCAGCAGACCCCGACTTCAAGTATGAGTTCCCTGAAGCGGTGGACTG
 CGGTAAATGTCAAGGTGACCTCCAACAGGCTTCCCTGCTCAGTCACTCCATCAGGATGTGCTGTCTGCTG
 TCTATGACCTGGACACAAACGTAGCCTTCACTCGGCATGTACACAGCATGACCAAGAGGCGCCATCACCGTAC
 AGCGCAAGACTTCCCGACGACAGCTTTATGTGGTGGTGGTGGTGAAGACCGAGACCAAGCCTGCGGGGGCT
 CCCTGCCTTTTACCCTTCGACAGAGATGACCCGGTGGTCAAGGGCACCGCGAGAAAACCTGTCACTGTCTGG
 TGTCTCAAGCAGTACGCTCTGAGGCATACGTCACTGGGATGCTCTTTTGGCTGGGTATTTCTCTCCTTTTACC
 TGCTGACCGCTCTCTGGCCTGCTGGGAGAACTGGAGGACAGAGAGAACCCCTGTGGTGGCCATTGACCGAG
 CCTGCCCAGAAAGCGGTCACTCTGAGTCTGGTGTATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCAGTGGGGACCTCTTACG
 GTTACCAGGGCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAAATGTCACTCGACCAAGCAATACCTCTATGTGGCTGACC
 TGGCAGCGAAGACAGAGCTGTTCTGCGGAAAAAGTACAGATCTACTCTGGAACATGCGCACTGTTCTGTCT
 TCTATGCCCTTCTCTGGTGACGTGTGTATCACTACAGACGGTGGTGAATGTACAGAGGATACGAGCACTCT
 GCTACTACAACITTCCTCTGCGCCACCCACTGGGCAATCTCAGCAACCTTCAACAACTCTCAGAACTGGGGT
 ACATCTGCTGGGGCTGCTTTTCTGCTCATCATCTCTGCAACGGAGATCAACCAACCCGGGCTGCTGCGCA
 ATGACTCTGTGCGCTGGAATGTGGGATCCCCAACACTTGGGCTTTTCTACGCCATGGGCACGCGCTAGTGA
 TGGAGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCAACTATACAATTTCCAGTTTGACACATCGTTCTAGT
 ACATGATCGCGGAGCTTCGATCTGGAAGCTCTACCAAGCGGACCCGGAATCAACCGCAGCGCTACAGTG
 CTAACGCTGCTGCTGGCCATTGCATCTTCTTCTGTGTGGGCTGGTCTTTGGCAGAGGGACGACGCGCTCT
 GGAATCGCTTCTTCCATTAATCATCATCGCAACCTGCTCCTCAGCACGCACTCTAATACGTGGCGGTGGA
 AACTGGAATCGGGATCTTCCGCGCATCTCCAGTGTCTTACACAGACTGCATCCGCGAGTGCAGCGGCGCG
 TCTACGTGACCGCATGGTCTGTGGTTCATGGGCAACGTCATCACTGTGCTGGCTGCTTATGCGGCTTATCA
 TGGCGCCCAATGATTTCGCTTCTACTTGTGGCAATTGGCATCTGCAACTGCTCTTACTTGCCTTCTACA
 TCACTCATGAAGCTCGGAGTGGGAGAGGATCAAGCTCATCCCTCTGCTGCTGATCTTGTGCACTCTCGGTGTCT
 GGGGCTTCGCGCTCTTCTTCTTCCAGGGACTCAGCACTGGCAGAAAAACCTCTCAGAGTGCAGGGAGCA
 ACCGGGACTGCATCTCCTCGACTTCTTTGACGACACGACATCTGGCAGTCTCCTCTCCTCATCGCATGTCTG
 GCTGCTTCTGGTGTGCTGCACTGGATGACGACCTGGATACTGTGAGCGGACAGATCTATGTTT**TAGC**
 AGGAGTGGGGCTTCTGCTCACTCAAGGGGGCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTGTGCT
 GTGGGATGAGTCCAGCACCGCTGCCAGCATGGATGGCAGCAGGACCGCGAGTCTAGCTTAGGCTTGGCT
 GGGACAGCATGGGTGGCATGGAACCTTGACAGTGGCTCTGCCAGGAGCAGCGCTGCTCCCTGGAAACCCCC
 AGATGTTGGCCAAATGCTGCTTCTCAGTGTGGGGCTTCCATGGGCGCTGTCTTTGGCTCTCAATT
 GTCCCTTTGCAAGAGGAGGATGGAAGGGACACCTCCCAATTCACTGCCTTGCAATTTGGCGCTCTCTCCGCC
 ACAATGCCCAAGCTGGGACCTAAGGCTCTTTTCTTCCATCTCCCACTCCAGGCGTAGTCTGGGGCTGA
 ATCTCTGTCTGTATCAGGGCCCAAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCAATTCAGTCAAGC
 AGGATGGATGGGGGTATGAGATTTTGGGGTGGCCAGTGGTGGCCAGACTTTTGGTGTAAAGGCTCAAGGGG
 CTTGGGCGAGTGCATTTCTTTCCCTCTGACGTGTGTGAGGGCTGGCTCTTTAGCAATGGCTCAGCCCAATT
 TGAGAAACCGCTTCTGATTCAGAGGGCTGAATTCAGAGGTCACTCTTCACTCCATCAGTCCACAGATGAGC
 AGCACCAGGAGTGGAGGGGAGAGCGCTCACCCTTCCCTTCTTCTCCAGGGCTTATGCTTGGCAAAACCC
 AGCTGTGGCTTCTAGTGCAATTGACACTGCCCAAGAAATGTCCAGGGGCAAGGAGGATGATACAGATTGAG
 CCGCTTCTGCTTCACTGTGGGACCCCGAGTGCCTACTAGAAAGGGGCTCAGGAAGGAGTGTGCTGTTT
 CCTCTACGTGCCAGTCTAGCTGCTCTAGGACCCAGGCTGGCTTATAGTTTCCGTCAAGTCTCAGGCA
 AGTTCTGTGTAGTCACTGACACACATACCTATGAACCTTGGAGTTTCAAAAGAAATGCCCGACGCTCGGGAC
 CTGGCAGCCCTGGTCTTGGATCCCTCTGCTCCACCTGGTCCACCCAGATGCTAGGATGGGAGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGGAATGTGTTTTCTCCAAACTGTTTTATAGCTCTGCTTGAAGGCTGGG
 AGATGAGTGGGTGTGGATCTTTCTCAGAGCGCTCATGCTATGTTGCAATTCGCTTTCTATGAATGAATT
 TGCATTCAATAACAAACGAGATCAAAAAA

2007/5/27 12:13:01

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLVLPKNVVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFORKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSPLFFYPFAEDEPVDQGHRQKTLSSLVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPESGHPRVLADSPFGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLKKYQIYFWNIIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHGFLFYAMGTALM
MEGLLSACYHVCNPNTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLLTSLQYYMGRWKLDGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSEFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCCTGTCCCTG
 ACCATGGTGCCTTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTTATACC
 TGACCAAGTTGCCGCTGCCCGGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAAGGGGACTCA
 GGCAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAAG
 GGCCTTGACCCAGAGGAGCAGGCAGAGTACCAAGTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCAGTGAAGGATGAGAATGACCAAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCTCTTCCCTTGAAGGCTTCAAGCCGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATGCTGAGCCAGGCTCCAGCCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAGC
 CTACCAAGCTGTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTTATACCCGCACACATGGCCCCAGGTACACTGGAGTGGGGGTGATGT
 GCACATCTCACCTGGAGAGCCATCCCCCGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCCAGAGAGCTGGACAGAGAAGCCCAAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATTGGCGAGGACTATCGGCCCTCTGGAGCTGCACGTGCTGGTGTGATGGATGAGAA
 TGACAACGTGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTAAGTGAAGTACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCAATTCC
 CAGCTTGTGATTCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACCA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCCGACAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT
 TGGGCCATAAGCCTCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCCCTTCCGCTCATGGATTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTAGACTCAGACTCTGCAC
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGGCA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCAGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCAATGCCAAGTTGGACAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGGCCCCAGCCTGGGGACACCTACACGGTCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTATCGTGAGTGGACCAAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTTT
 CCATGCTTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCTGCAAC
 GTGGAGGGGACAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTCCGC
 AGTGGGCATCCTTGTAGGCACCTTGGTAGCAATAGGAATCTTCCTCATCTCATTTCACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGGCCCTGAAGGGC
 ACTGTGCTCAATGCCCCAGGCAGCTCTAGCTGGGAGCTTGGCCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCCACCAAGATCCAGCAGGGGACAGGACAGGATAGAGAGGCCCTCCAT
 CTGCCCTGGGGTGGAGGCCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGGCCAATAATTAAGCCCCA
 GAGAAGTGGGCTGGGCCCTGGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

FIGURE 132

MVPAWLWLLCVSVQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQFVLVHVKDENDQVP
 HFSQAIYRARLSRGRTRPGIPFLFLEASDRDEFGTANSDLRFHILSQAPAQSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAE
 NLKVLVPHHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPFRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAFAQVDPTSGSVTLGVPLPRAGQNILLVVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV
 MPPPKLQDES YEASVPISAPAGSFLTTIQPSDFISRTLRFSLVNDSEGWLCEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGNPTVQRDWRQLTLNGSHAYLTALHWWPEPREHII PVVVSNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTLVLAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACGTGTTTCATGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAATCTCCCTCCTCT
 TCAATCGGCCTGTGGATGTCTGCTGCCATCTGTGAGTCCGAGGCATTTAAATCCTTCCCTG
 AGATCCAGGGCCTTAGATACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAAATGA
 AGATGATGAATGCAACCAATGAAGGGCAAGAACGGAGCAGTAATACTTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAGAACCGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAAGCGCGCCGCCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTCTTGTTCGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTGTGAGGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAGTGATACCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCCCAGATGCC
 GAGAACTCGCAAGTTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTTCTGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAAACGGCATCAAATTTGATTACATTTGAGTTGAGAGATACCGGAGCATGTGGC
 TTCTCTCTGCCAGTAAACAGATCATCCCCACTGCAGAGGAGAGCTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTTAGCGGATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CTGTTGTCCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCAGCGCTGTCAATTTTGGTCTGT
 CTGTTTTTGATGAGCCTTTTGTCTGTTTCTCCTTCCACCTTGCTGGCTGGGCGGCTGCACTC
 AGCATACCCCTTCTCGGTGGCATGTCTCTCTACCTCATTTTGAACCAAAGAACATC
 TGAGATGATTTCTACCCCTCATCCACATAGCCAAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAAATTCCTTTAATTTCT
 TCGCAGTCTTCTGGAATAATTTTCTTTGAGCAGCAAACTTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTGTCTTGTGTGCC
 CAGGCTGGAGTGTGATGGCTCGATCTTGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA
 ATTTCTCTGCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTTGTGTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGCCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TCGCGGCCGCTCCCTCCTTTTATAGGCTGAATACAAAGTAGAATCACTTTCCCTTAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTATTACAGTGTG
 ACCAGGTGGCGGAGGGGATCTGTGTCTACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTCAGGATGGTGAATATTATCCCATCTGTCTTAATGGGCTTACCTCTCT
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT
 CTGGCTGGTAATCTCACTGCCCTGGCACATTCCTTTGTGCTGTGGTGTATCCTTCCCTGTT
 TCCTTGTCTGTTTGT
 TCTGTCTAATTTGATCTGGACCACAAGTTCTCAAGTAGAGCAAGAATGTGACCAACAGCT
 GCCTCTTGTTCATTTCACTCAGCACGTACCATCTGTCTCTTTTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTGCTTTTACCAAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACAC
 GCATCTGGTGTGCTTTATAAGCCAATAAATATTCATGTGAAAAA

1001757-13301
 TCGGCTT-25-1001

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

[illegible]

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSA LFVKELQLQANFLGNVKRLYEAEVFSTDFSNP SIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCG
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
 CCTTTATCTCTTCCACCTTCAAGTCCCCTTTCTCAAGATCCTCTGTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCTCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACTCTCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTTCCA
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAAGCAGCTCCAATGGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGC
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAACTCTCCAGTGGGGCCGGCAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGGATCAGCACAGTCCACCAATCTGAGTCCAGCACACCTTCCAG
 TGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCTCAGTGGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGGATCAGCACAGTCCACCAATCTGAGTCCAGCACAACT
 TCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGGGCAA
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTTGGTCTCGGTTGTGGCG
 GCGCTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
 CTTTAACACAGCTGTCTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCACAGGCCAGGTGGAGTCCCTAACTGGTCTGGAGGAGACCAAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAGCAGCCCCGAAGCAAG
 TGCCGATCTCTCAGGAAGGAAGAGACCTGGGCACCCAGACCTGGTTTCCCTTTCATTTCATC
 CAGGAGACCCCTCCAGCTTTGTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTCCACC
 TTTCTTGCTTTTACCAGACACTGGAAGAGAAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCGGGGTGGGTATCTAG
 CTCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAATCCAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVT SNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSESTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNESSESTVSSRASTATNESSESTLSSGASTATNSDSS
TTSSGASTATNESSESTTSSGASTATNESSESTVSSRASTATNESSESTTSSGASTATNESRST
SNGAGTATNESSESTTSSGASTATNSDSSTVSSGASTATNESSESTTSSGASTATNESSESTTSS
GASTATNSDSSTTSSGAGTATNESSESTVSSGISTVTNESSESTPSSGANTATNESSESTTSSGA
NTATNESSESTVSSGASTATNESSESTTSSGVSTATNESSESTTSSGASTATNSDSSTTSSEAST
ATNESSESTVSSGISTVTNESSESTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGHAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGACGCTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
ATGCCGGAAGGGGAAGTGGAGAAGGTTTTCAACGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTA CTG
GGATTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

TCCGGGTCCCGAGGGGCTACGTCGGCGGCGGCTGGCCAGGGGAGCAGTCAGTGGACACTCCAGGAGAGCGCG
 CGCGCGGGGGGATGACGCTGGCTGACCTTCACTCACTCACTCGGAGCGGGGGCCCCCGGGGCGACTCG
 GGGGCGGAGCCGCGGGCGGAGCTGCGCCCGTGAGTTCGCGCGAGCCACTTGAGCCGAGCGCGCGGACACCGTCT
 CTCTCTGCTCTCCGAATGCTCGCCAGCGCATGGGCTCGAGGAGCTGGCTCGCGGCCATGGGGCGGGCTCGCG
 CTTCCGCGATCGCTGCTGCTCTCTCTGCTCTGCTGCTGCTGCTGCGAGCCGCGCTCCGACACTGGGCGCTCAGC
 CCGCGATCAGCCTGCTCTGGGCTCTGAAGAGCGGCGATTCTCAGATTGCAAGTTCAGACATCTCCAATCA
 ACAGCGCTCTCTCTGAGCAGGGATGGCAGGACCTGTACGTTGGGTGCTCGAGAGCGCCTCTTTGCACTCATGAC
 AACTTCAGCTTCTCGTGGAGCGGGGATACACGAGAGCTGCTTTGGGTGCAGACCGCAGAGAAACAGCACTGC
 AGCTCTCAAGGCGAGACCCACAGCGCATCTCAAAATCACTCAAGATCTCTCTCGGCTCAGCGGCATCTCT
 CTCTTCACTCTGGCAGCAGCCTCTCAGCCGCTGTGTACTACATCACTAAGAGAACTCAACCTCGGCAAG
 CACGAGAAGGGGATGTCTCTCTGAAATGGCAGGCGCGTGTGCGCTTCGACCGAAATCTCAAGTCCGACTGCC
 TGGTGGTTGAGTGGCGATCTACACTGGAACGTCAGCAGCTTCCAGGGGAATCAGCGGCATCTCGCGAGC
 CAAAGCGCTTGGCCCCACCAAGACCGAGAGCTCTCTCACTGGCTGCAAGACAGCTTTTGTGGCTCAGCTAC
 ATTCTCTGAGAGCGCTGGGCGACTTCGCAAGGCGATGATGACAGCACTATCTTTTCTCAGCGAGACTGCCAGGA
 TTGTAGTCTTTTGAGAACACATTTGTGTCGCGATTCGCCGATCTCGAAGGCGGATGAGGCTGGAGAGCGGGT
 CTACAGACAGCGTGGACTCTCTTCTCAGAGGCCAGCTGTGTGCTGCTGCGCCGAGATGGCTCTCCCTCACT
 GTGCTGCAAGATCTCTCTCAGCTCGACGCCACCGAGGACTGGGCTGACGCCCTTTCTATGGGCTCTCACT
 TCCGACTGGCAGAGGAACTACAGAGGCTCTCGGCTCGAGTGTCTCTCAAAATGAAGATGTGCGAGAGTCTCT
 AGCGGCTCTACAGAGGATGAACCGTGCAGACAGCGATGGTACACCTGTACCACCCGGTGGCCACACCCGCG
 CTGGAAGCTCACTCACCAAAGTCCGCGGGAAGGAAGAACTCACTCATCTCTCGAGCGCTCCAGACCGCGTGTCT
 AACTTCTCTGAGACCACTCTCTGATGAGCGGCGAGCTCGAAGCGCATGCTGCTGTGCGACGCCAGGCTGCT
 TACCGAGGCGCTGAGGCTGATACAGCGGCTCTCGGCTGCGACACACATCAGAGTGTCTCTCTCTGGGCACTGTGATG
 GCGCGGCTCCAAAGCACTCAGCGCTGGGCGCCGGGTGCACATCATGTAGAGTCTGCAGTCTCTCATGGGA
 CAGCGCCGCTCGAAGATCTGCTCTGCAAGCCACAGGGGGCTGCTGTATGGGCTCACTCTCGGCGCTAGTCTCAG
 GTGCGCTATGGCCAACTGCAAGCTGTACCGAGTGTGGGGATGCGCTCTCGCGCGGAGCCCTCATGTGCTTGG
 GCGCGCTCCAGCTGCAGACAGCTCAGCCTCTACACCGCTCAGCTGGCCACAGGCGCTGATCAGGAGACTCGAG
 GGAGCGAGCGCAAGAGCTTTGACGGCGTCTTGCTGGTTGTGTCGCTCTTTGTATCAACGGAGGAGAGCA
 TGTGACCAAGTCTCAGTTTCAGCCGCAACACAGTGAACACTTTGGCTCGCGCGCTCTCTCAACCTGGCGACCGGA
 CTCTGGCTAGCAACGGGCGGCGGCTCAATGCTCGGCTCTGCGACGTGTACCACTGGGAGCTCTGTGCTGT
 GTGGGCAACCAAGACTGTGGGAGTTCAGCTGCTGTGCTAGAGAGAGGCTTCCAGACGCTGGTATGAGCAGTAC
 TGCCAGAGGTTGTGGAGAGCGGGGTGCGAGACAAGAACAGTAGGTTGGGAGTGTACCGGTACTATTACAGCTA
 TCGGTTGTGATGCACCAAGCTGGTGGCAAGGCGACTGGGTTGCGACAGGCTCTACTGGAAGGAGTGTCTGTGT
 ATGTGACAGCTCTTTGTCTGCGCGCTGCTGCTCCAGTTTATTCTTGTCTACCGCAGCGGAACAGATGAAGA
 GCTCTCTGAGCAGCGGGGAATGTGCAAGCTGCACGCCAAGAGCTGCCCTGGTGTGCTGCCCTCTGAGCCGCG
 CCACTCTAGGCGCTAGGCGCCCTTAGCACCCTGCTGATACCGAGGGTTACAGTCCCTGTACAGACGCCCCG
 GGGGCGCGAGTCTCTCAGTATGAGCAGAGAAGGCCACTCAGCATCGAAGACAGTCTGTGGGAGGATATCCCAAT
 TCGCCCGCGCGGGTGCCTGTGGCTGGAGATCCGTGACTGTGTGCTGTGAGAGCTGACTTCCAGAGAGCT
 TGCCCTGGCTTCAGGGGCTGTGAATGCTGGGAGAGGTTCAACTGGACCTCCCTCGCTCTGCTCTGTGGAAC
 ACAGCGCTGGTGGCGGCGCTGTGGAGGCTTTGAGACAGCTGGGCTGTGCTCTCGATTGAACTAGCAGAGCCCTC
 TACACCCAGACACCCAAACAGCGCTGGCCCAAGAGCTCTGGCCAAATATGGGGCGCTGCTAGGTTGTGTGGA
 CAGTGGCTCTTATGATAACTGAGGCTCTTTGTTAAATAAACAATCAAAATGTGAACTAGAATGAGAGGAGAA
 ATGACATGGCATCAGACACACAGCGCTGTCCAGTTCTATGCGCTCCGAGGGGTGCTGGGAGTGCATCTCAAATGG
 TTGCTGTGAGACAGATTTGAAACCTCTCAACATGGGCTCTCTCACTTCCAAATCTCCGCTGCGACCGCTGCG
 CTTGCTCTCACTCGAGATCAGGACCACTGTGGGCTGGCTGGTCTGTGCTTGCACCTCAGCGAGGAGTGTAGTTG
 TTGCTGGCTGCTGCCAACACTCAGGACAGGAGGCTAGGTTGGCATCTCGGCGCTCACCAGTCTCTGGGCTCT
 GGACCCAACTCTGGACCTTTCCAGGCTGTATCAGGCTGTGGCCACAGAGGACAGCGCGACTCAGGAGA
 TTTGTGTCAGATGTAGCGCTTTCTCTCAGTAATCAGGGAAGAGACTGCGCTGCTTCTCTCGTTGTGTGCTGA
 GAACCCGTTGCGCCCTTCCCACTATCCACTCGCTCATCTTTGAACTCAAAACAGGAGAACTCACTGACC
 CTGGTCTCTCCCGAGTCCCGAGTTCACTCTCATCGCTCACTTCTCTCACTCTTAGGAGATCACTCAACTGCCC
 AGCAAGGGGCCCCGAAATTTATGTGTTTTTATACATTTTTTAATAGAGTCACTTTATGTCACTTTTATAAA
 GCTCGAAGAACTACTGTTTAAAAAATAAAAA

FIGURE 142

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPILLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQCCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSSQGNDPAISRQSRLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPLHHTYDVLFLGTGDGRHLKAVSVGPRVHII EELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRFPWIIDIEGASAKDLCSASSVVSFVPTGEKPCQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTQQLGFEQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVFLFLYRHRNSM
KVFLKQGECA SVHPKTCPPVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPVRVLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

[illegible]

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCAATGGAGGGCTGCGTATTTGTAAATAG
CTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTGTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAAA

FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVIPVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQIGIPPSFMRFPQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKINILIPLSGRFDMFVRFMGNFECTC
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESILLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEVDVLEFNKVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGCTCG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTAGCAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAAACCAATCCTATCAGTGAAGAAATACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAACTGCCATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCAACAAGTGCAACAGGCACCTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC
 TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAAATTTTAAACCTACTTGATATTTCCATAACAAAGCTGA
 TTTAAGCAAACCTGCATTTTTTACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGGTTTCAGGAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
```

```
><subunit 1 of 1, 350 aa, 1 stop
```

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
 HVYSIASKGSKFELVTHGDASTENDVLNTPISEETTFPTGGTFPEIGKKKHTESTPFWSI
 KPNNVSIVLHAAEPPYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
 STGIEISTESEDVPLSGETAIEKPEEFGKHPKSWNNNDILKILKIDINSQVQQALLSDTSNP
 AYREDIEASKDHLKRSLAALAAAEHLKTKYSQLLPVGRTSNKIDIDTETVINMLKNSRSKL
 YEYLDIKCVPPEMREKATVFTLKNMCRSRRTALKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCACAA
 GGAATATCC**ATG**GGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACGGGCAAGTTTGTCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGGGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGC
 TAAAAAATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCACAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCATTTCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTTGTGTTCCATCCACCTTGCTGAGCAGAGTCAATGAGGTGGAATCCAAGGTATTTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGAAAAATCCA
 GGCGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACAG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAG
 AAAATGATAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGGAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTTAC
 ATTTCAATCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
 GGAAGAGGGGACTCCCATATTTATATGTCCAGTGTCTTGGGGAT**GA**GACAGAGAAGACCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTCTTCTGCGCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
 TGGCTTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTGTGTTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTGTGCTAGTCACGGACAGTGATTCTTGCCCTCACAGGTGAAGATTAAGAGA
 CAACGAATGTGAATCATGCTTGCAAGTTTGAGGGCACAGTGTGTGTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACCTCTGTTTGCTTATTCCACATTAATTACTTTTCTCTA
 TACCAATACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTTCTACTGATTCTATAAGCCCAAGCATTACCTGATACCAAAACCAGGCAAG
 AAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAAACACAGACAAAAA
 TTCTAAATAAAATTTTAAACAATTAACCTAAACAATATATTTAAAGATGATATATAACTACT
 CAGTGGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGGTGAATT
 CAGCACAATTAATAAGTAAAAAGAAAACCATAAAAA

1007527.34701

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQFSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELEDWRKKGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGA AAAATGCAATTTTATAAA
 TCTCCATTAAAGGAAGAAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACCTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTA AAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGCTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAAG
 CCTGGTGTGTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAAATGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTGTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGACGTAAGCATCCTGCCTCTG
 CCAGATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCACTTTGTTCTCTAGAAGTTTGTGAGAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTTCAGTTCCCTC
 AGCTCCTCTCATTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAAAGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTCATATTTTATTTGGCACAGAAAAGTATTAGTGTTTTCTCTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAATAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACCTTCATGCAATGTACTTGTCTTAAGCAAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSFPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCTCAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCTTGGCCGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCCG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCCTTCGGGCCTTGACCCGCTTGGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
 GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCATCGCTGGGGCTGCCCGCGCCGAGCCGCCCGAGCCGAGGGCGCTCTGA
 AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
 GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA
 AGCGGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSFCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAFFSPVLHYWLLLDGSEA
AQKGPEPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDRWGCPRRAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGG
 CCCAGCGCCGACGATCGCTGCCGTTTGGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACATGCCAGAGAAGATTCCGTGAAGTGTCTGCCCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA
 TGAGGGACTACCTAAAAAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTG
 ATTTTGACTTACTTTCTGTGGTTTATCCGGTCATGATTGCTGTTTGTCTGTTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCACTTTCTGTGTAGAACCTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACCTTATGGTCCAGTACAATGGTCAGATATGGTCACTTTGAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGTTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAAATGTATTCCTTTTGAAGAGAACCAACAACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGATGACAACCTCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAACCAAGCC
 TGTCAAGAACTCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAAAAAGAAATGTACAGAGAAGAAACCACAACTGTTTATTGGACTTGTGAAT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAGTTTCTATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTGAAGCAGCATGGTTTGATTAGCAATTC
 CGACTCCATGCCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACTTTT
 AATATTGGTGACTACCTAAATGTGATTTTGTGCTGTTACTAAAAATATTCTTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTTAAA
 TCTGTATAATTGAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCTGTATAGCATCATTTTATTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATACTGTTATTAAATACTTAACCACTAATTTTGAAGAAAT
 CCAGTGTGATACATAGGAATCATTATTACAGAAATGATGCTGGCTTTTAGGAAGTATTATAA
 GAAAAATTTGCACATACTTAGTTGATTCAGAAAGGACTTGATGCTGTTTCTCCCAATG
 AAGACTCTTTTGCACATAACACATTTTAAAAAGCTTATCTTTGCCCTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAAATAGTGTTCTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACATGTGACAAATTAAGAGATCTTTGTTTTATTTACATGATTA
 ATAACTGTGGCAAAATACACAGATTATTAATTTTTTACAAGAGTATAGTATATTTATTT
 GAATTTGGGAAAAAGTGCAATTTTACTGTATTTTGTGATTTCTTTGTTTTATTTCTCAGAAATAGAA
 AGAAAAATTAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCGTGCCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**CATGT**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATATTGTGGTTGTCTCATCAAGG
 TGATTCTGGATAAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCGCT
 GTGGTGGGTGGGGAGGAGGCCCTGTGTGATTCTTGCCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCTACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCACTCCA
 GGTCAATTGACAGCACACGGTGAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCCAAGGATATACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCTTTGCAGTGCTGGGAGCCGCTTCTTCTCTG
 CCTGCCCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCTGCCCCACAGCCTCAGCATTCTTGAGCAGCAAGGGCCCTCAATTCTGTAAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTCAACCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTGTGAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACTCT
 CTGGCAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEEASVDSWFPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGF TKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMM CAGIPE
GGVDTCCQGD SGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGAAACGACGGGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGGCTCCTGGGGC
TTTTCTCTTCCAAGTCTTACGTGCTGCTGCCAGCAGCAGCCGGGGGAGGCGGGCAGGGGCCATGCCA
GGTCCAGATCATGTAGCAGGGGTAAGCTAGGGCACTTAGCTTCTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGATGGAATACTCTCTACGTGGGGCTCGAGAAGCATTCTGGCCTTGATATCCAGG
ATCCAGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCTTTA
AGAAGAAGAGCAATGAGACAGAGTGTTCACCTCATCCGTCTCGTTCTTACATATGTACCCATCTCTACA
CCTGCGGCACCTTCGCTTCAGCCCTGCTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCATCTCGG
AGGCATAGGTCTATGGAGGAAAAGGCCAAGCCCTTTGACCCGCTCACAGCATACGGCTGTCTTGTTGGATG
GGATGCTCTATTTCTGTACTATGAACAACCTTCTGGGCACTGAGCCCATCTGATGCGCACACTGGGATCCCAGC
CTGTCTCTCAAGACGCAACTTCTCTCGCTGGCTGCATCATGACGCTCCTTTTGGCAGCCATCCTTCGACCC
AGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGG
CTAGAGTCTGCAAGATGACGTGGCGGCGGAAAAGCTGCTGCAGAGAAGTGAGACCCTCTCTGAAGGCCCGAGC
TGCTCTGCACCCAGCCGGGCACTGCTTCAACGTCATCCGCCAGCGGTCTGCTCCCGCCGATTTCTCCA
CAGCTCCACATCTACGAGTCTTACCTCCAGTGCGAGGTTGGCGGACCAGGAGCTCTCGGTTTGTGCT
TCTCTCTCTGGACATGAAGCTGTCTTTAAGGGGAATACAAGAGTTGAACAAAGAACTTCAGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCACTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCT
TCATGAAGGCACTTCTCTGATGGATGAGCAAGTGTGGGACGCCCCCTGCTGTGAAATCTGGCGTGGAGCTATA
CAGGCTTTCAGTGGAGACAGCCAGGCGCTTGATGGGCACAGCCATCTGTATGTACCTGGGAACCCACAG
GGTCGCTCCACAAGGCTGTGGTAAGTGGGACAGCAGTGTCTCATCTGTTGAAGAGATTGAGCTGTTCCCTGACC
CTGAACCTGTTGCAACCTGACAGTGGCCCCACCCAGGCTGAGTGTGTTGATGGCTTCTCAGGAGGTGTCTGGA
GGGTGGCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTTGACTGTGTCTGCCCCGAGCCCTCAGCTGTGCT
GGGACCTGAGTCCCGAACCTGTTGCTCTGTCTGCCCCCAACCTGAACCTCTGGAAGCAGGACATGAGCGGG
GGAACCCAGAGTGGGCTATGTCAGTGGCCCATGAGCAGGAGCCTTCGGCTCAGAGCCGCCGCAATCATT
AAGAAGTCTGGCTGTCCCACTCCATCTGAGAGTCCCTGCCCCACCTGTGAGCTTGGCTCTTATTATT
GGAGTCATGGCCAGCAGCAGTCCAGAAAGCTCTTCCACTGTCTACAACTGGCTCCCTCTGCTGATAGTGCAGG
ATGAGTGTGGGGTCTCTACAGCTGTGGGCACTGAGAATGGCTTTTCATACCCTGTGATCTCTGATGTTGGTGG
ACAGCCAGGACCAGACCTTGGCCTGGATCTGAACTGGCAGGACATCCCCGGGAGCATGTGAAGTCCCGTTGA
CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTGCTGTCTGCTGTCTCT
TTGCCTTAGTCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATGAGAGCACTCCGGGCTCGGGGCAAGG
TTCAGGCTGTGAGACCTGCGCCTGGGAGAAGGCCCGTTAAGCAGAGAGCAACACTCCAGTCTCCCAAGG
AATGCAGGACCTTGCCAGTGTGAGAGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
CAGGCCGGGCTGCGGTGACGACCTGGCCATGCTGGCTGGGCGGCCAAGCACAGCCCTGACTAGGATGACAG
CAGCAAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGATGACACTCAGCAGGGT
ATGCACAGCAGTCTGCTCCCTATGGGACTCCCTCTACCAAGCAGTGAAGTCTCTAACAGGCTGGGGCTAC
CCCCAGACTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCGAGGACCTTC
CAGAAACAGTGTCTTCAAGAGACCTTAAAAAACCCTGCTGTCCAGGACCTTATGGTAATGAACACCAACATC
TAAACAATCATATGCTAACATGCCACTCTGGAACCTCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTTACAGTCTGTCACCGCTGACTCCAGGAAGTC
TTTCTTGAAGTCTGACCACTTTCTCTTGTCTCAGTTGGGGCAGACTGCTGCTCTGCGCTCTGCGCTGGCAGATGG
CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTACCTCTCCCCCTCCCTTTTCTTTGT
TTTGGGATTCAGAAAACCTGCTGTGAGAGCTGTTTATTTTATTAATAATATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
 ><subunit 1 of 1, 761 aa, 1 stop
 ><MW: 83574, pI: 6.78, NX(S/T): 4
 MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMRVRVRYAGDERRALSFFHQKGLQ
 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC
 FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHATA
 VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAaipSTQVVYFFFE
 ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
 PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
 NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
 YLGTTTGLSHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAIVGFGSGGVWRVPRAN
 CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
 QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPVEASSTVYNGSLLLIVQDGVGG
 LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
 HFVTVTVLFALVLSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
 SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGCATGGCTGGGCAGCGAGTGTCTCTCTAGTGGGCTTCCCTTCTCCCTGGGGTCTGTCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAGAGAAATTTAAAAAGAGTTTGGATTCTTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAAATTTGAAAATTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAAATGAGAATCTGCATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
 CAGTATCCGTTCTTGTGCTGACTGATCAGATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAAACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTGACTTTGCTTTGATTTTGTCTGCACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGCG
 CAAGTTTGGGACTCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACTGTGAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTCTCATTTGGCCCAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGTGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGCTGTTTGTCAACCCACGGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTGCTGCCCTCCACCCGCTCAGGCCCCACACAG
 CGGCTGGTGGGCTGGAATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA
 TGTCTTTTCAAGACCCCTGGCATGAGCAGTACCTGTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCACCAATTTCTAGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTTCCAGTCCT
 CTTGTCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTAGTGACTTG
 GACCCTGACCCCTCAGATTTCAGCCTTAAATCCACCTTCTCTCATGCGCTCTCCGAA
 TCACACCCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGATATTTCTTTCAGTTTCTGTTT
 TGTCTTCCACATTTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAAGATTTCAGGCG
 CGGACACAGGCTCAGAGTCTCCACATTTGGTCCCTGTCTCTGTTGCCACAGTGAGTCTCT
 TCTTGGCTGAGCGGATGAGAGACTGAGTTTCCAGATTTCTGAAAAATAAAGTTTACA
 GCGTTATCTCTCCCAACCTCACTAA

10017527.121301

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKG
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKL GKPFVAILSTSFSGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWF
INSDFAFDFAFRLPNTVYVGGLMKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT
CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGTTTCATCCCTCCTTTCTCTCCCAAAGCCCA
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGC
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCAGA
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGAGCCCAAGCCACTGGC
TACCAGTCCCCTACACAGTCCCGGGCTGCCCTTGGTCTGGTGCTCTGGCCCTGGGGGCC
GGGTGGGCCCAGGAGGGGTGAGAGCCCTCCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
GAGTGGCATTGTGCGGTCGGAAGCCACCACATGAGCCAGCAGGGGAAACCGGCAATGGC
ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACAGGGGCGGTGGCTTTGACCGGGC
CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCGGGTTCCATGTGGTGAAGG
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCCTGTCTATCTCAGCC
TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGC
CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAATACT
CAAGTTTCTCTGGCTTCCTATCTTCCCTCTCTGAGGAGCCCAAGTCTTTCAAGCACAGAAT
CCAGCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCTGTGCCAAACACCCAAGTTTAA
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCTTTCCACCCACCCACCCCAAGTTACC
CTCCAGCCACCTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGGA
AGAAGGAAGATCTGCACTACTTTGCGGCCCTGCTCCTCCGGTCCCCACCCAGCTTCCT
GCTCAATGCTGATCAGGACAGGTTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCCTGAGGAAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCTTCTATGTCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
GGTGAGTGTGTTTCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATTGAAAACATCGATAACCATGCATCCTCTGCTTGGCCACCTCCTGAACTGCTCCAC
CTTTGAAGTTTGAACCTTGTCCCTCCACACTGACTGCTGCCTCCTTCCCTCCAGCTCTC
TCACTGAGTTATCTTCACTGTACCTGTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
CTGTGCTGTCTTATCTCTCTCTTAGGCTTCCTATTACCTGGGATTCCATGATTCATTCTCT
CAGACCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTCTTATCCCGCTGTCCCAT
GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCAGTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACATAAAATAAAAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEFVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGSFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPFVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGLIFPL

Signal peptide:

amino acids 1-32

FIGURE 163

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCTAGCCGCCAGC
 CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGCAT
 GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGCCGTGACTGGGCGGGCTTAGCCAT
GAAGACCTCATAGCCGCCTACTCCGGGTCTGCGCGCGAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTCAGGAGGACCTGCGCTGTGCGCGAGGGGTCTGGGAGATGGGGCACT
 GGATCCAGCATCTCTCCGCCCTCCAGGACCTTCTCTGTCACTGGCTCAATAGGTCCAA
 GGTGGAAGCAGCTACAGGTCACTCAGTGCTCCAGTGGGTCTGTCTCTCTTGTACTGG
 GAGTGGCTGCACTGCCATCTCATGTACATATTCTGCATGATTGTGGCTCATCGCTGTG
 CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCATCCAGCTGGTGA
 AGACACACAACCTGTGTGACCACCAGGAACCTATATCTTTGGATACCACCCCATGGTATCATG
 GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCAGG
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTGAGCCGGGACACCATAGACTATTGTCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCTGCGGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC
 GAGGAGGGCTCTGGGGCCGATGGGTCCAGAAGAAGTTCAGAAATACATTGGTTTCGCCCC
 ATGCATCTTCCATGGTCGAGGCTCTTCTCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCCTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG
 CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA
 CAAGACCAAGTTCGGCTCCCGGAGACTGAGGTCTGGAGGTGAAGTGAAGCCAGCCTTCGGG
 GCCAATTCTCTGGAGGAACCACTGCAAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGTCA
 TGGGTGTCTGTGGGTTATTTAAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAA

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAYLYFTWLVDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIIVGGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRLGFSSDTWGLVPYSPKPTTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKEGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

GGCGCGGGGATGSGGGCGGGGGCGCGGGCGCGCCTCGTGAAGGCCCGGACGACGAGGGCGGGCGGGCGCGCG
GGGCCGAGGAGCGCGCGGCCAGAGCGGGGCCGCGGAGGCGACGCCGGGAGCGCCCGCGCAGCAGCAGGTGCGCG
CGCGCTGCGAGGCTTGTCCAGCGCGAAGCCCTGAGGCGACGTTTCCACTGGCTCTGCTGACCTTGTGCCTTGG
CGGCTGTCTCCTCAGGAGGGCGCTCAGCCCGCTCTGAGCAGCGCATGCGGCTGCTGGCTCTCTAGAACCCCA
GTTCTGCTGCACTGCTGCTGGTCGGCTTTGTCTCTGTTGAGTGGTCTGTCATCAACTTCGTCAGCTGTGCAC
GCTGGCGCTCTGCGCGGTGACGAAGCAGCTCTACCGCGCCTCAACTGCGCGCTCGCCTACTACTCTGTGAGCCA
ACTGTCATGCTCTGGAGTGGTGTCTGCACGGAGGTACACTGTTACGGAACAGGCCAGCGTAGAGCGCTT
TGGGAAGGAGCAGCGATCATCTCTCAACCAACTTCAGATCGACTTCTCTGGGTGGACCATGTGTGT
TCGCTTTCGAGTGTCTGGGAGCTCCAAAGTCTCTCGCTAAGAAGAGGACTGCTCTACGTGCCCTCTCATCGCTGGA
GTGGTACTTTCTGGAGATTGTGTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
GCGCCTGTGCGACTACCCGAGCTACATGTGGTTTCTCTGTACTGCGAGGGGACGGCTTCACGGAGAACAGCA
CCGCGTTAGCATGGAGTGGCGGCTTCAAGGGGCTCTGCTCTCAAGTACCACTGCTGCGCGGACCAAGGG
CTTACCACCCGAGCTCAAGTGCTCGGGGGCAGTTCGACGCTGTATGATGAACCCCTGAACTCAGAGAAA
CAGAAGACCCGTCCTCTCGGGGATCTCTACGGGAAGAAGTACGAGCGGCATCTGTGCGTGAGGAGATTTCCTCT
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACAGGAGAAGGACGCGCTCCA
GGAGATATATATATCAGAAGGGCATGTTTTCAGGGGAGCAGTTAAGCCTGCCCGAGGCGGTGGACCTCTGAA
CTTCTCTGCTGGGCGACCATCTCTCTGCTCCCCCTTCAGTTTGTCTTGGGCGTCTTTGGCAGCGGATACG
TCTCTGATCTGACTTCTTCTGGGTTTGTGGGAGCAGCTTCGTTTGGAGTTCCGACGATGATGAGGAATCGCT
TGAACCTGGGAGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGACGAGCT
CAGTCTCAAAAAAAAAAAAAAAAACAAAAAAAAAACCCAGAAATCTCGAGTTGAATGTGTAGTTACTGACATGAAA
ATTCTAGTAGGCTGAACAGCAGATTGTAGCAGGCGAGAAAAAATCAGCAAGCTTGAAGATGTACTTTTGATATT
TTTCAGGCTAATGAAAAAGATGAAGGAAATTAACAGCTCAGAGACCCATGGTGACCCGTACACAAATCAA
CATATGATGATGAGATCCGAAAGGAGGAGGAGAAGGGTCAGAAAGATGGCCACAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCA
AATCAAAGTGTCAAATGACAAAGATCTTGAAAGCAGCAAGCAGATGAGCAACTATCTTGTTCAAAGGATCTTGT
ATCAGATTCAAAGCTCATTTTCTCTCAGAAATCATGGAGGAGGAGGAGATGATTTGGATGAACACTGTTGAAGGCA
AACCTTCAACTGTAAATATTGACATTTGAGTCTTGAGTGGCTCACTGCTCTTTGGTCTCAGGCTGTTTTCAC
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGAACCTTAGGAAGGCCTGTCTTTAGGCGGGGCACAGTGG
TTACACCTGTAATCCAGCACTTTGGGAGGCCGACAGCGGTGATCATTTGGGGTCAGGCTGATCTCAAATCCT
GAGTTTCAGGTGATCTCGCCGCTCAGCTCCCAAAGTGTGTTGATTGACGGCGTGAGCCATCGCCTGCGCCGA
ATTCTTTTAAAGCTGAATGATGGGGGCGAGCAGATGAGCTCAGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACACATCGCTGGCTAATTTTGTATTTTAGTAGACAGCTGTGTAGCAGGCTGGTCTGCATCTCT
GACCTCAAGTGACCACCTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCCTTGA
GCATCTTGTGATGTGCTATTATGGCCATTGTATATCTTCTATCTTTTGGGGAATGTCTGTCAAGTCCCTTG
CCTTTTAAATTTTATTTATTTATTTATTTATTTTGTAGACAGGGTCTGTTCTGTGCGCAGGCTGGAGTA
CAGTGGCAGAGTCTTGGCTGATCAGCCTCGACCTCTGGGTCGAGTCTTCCACCTCAGGCTCCCTGT
AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
TGCCAGGCTGGTCTGAACTCCTGAGCTCAAGTGATCTGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
CATGAGCAGCTGCACCTGGCAACTCCAAAAATCAACACACACACAAAAAACCACTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCAGGCTG
CAGTGAAGTCAGGTTTGTGCAGTCACTTCCAGCTTGGACACAGAGTGAAGCCTGTCT

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVGLVINQVQLCTLALWVPVSKQLYRRLNCR LAYSLWSQLV
MLLEWWSCTECTLF TDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKRR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGGK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLITFLGVGAASFVRRRLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTTAAGAATCTGAAGTACTATGCCATCACTCCCTCCAATGTCTCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTAGAAGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTGTTCTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTTCTCTACTTAATATGTAGTC
 ATCCTGCGAGATTTCAATTCTAACATCATTCTTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGGCGTAGGGTCAAGGGCATTGCTGTGCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTATAGAGCTAAATGGAGGAGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTGATTAGTAGGCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGCC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHILCVCFSPALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIREPWVRR
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHITLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCCTCGAACAACTTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAAGTCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCGTACCTAC
ATTAATAATCTGTTTTTGTTCCTCTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCAGTACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGGTA
GCTGCGGCTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGCAAGCCCCGAAGATTT
CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATACGCTGCCCGCCCAT
CTAACCTTTTCATGTCCTGCACATCACTTGATCCATGGGCTAATCTGAACCTGTGCCAAG
AACCAGAGGCTTGAGTACCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACTGGTT
TATGTGACAGGATTGCATGCTTCCCTGGAACATGAGGGAAGCCGGAGAAAGCAAGTGGCA
GGGAAGGAACTTGTGCCAAATATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
ATCGAGTCTCCTGCATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCCTCCCCTCCTTCCCTC
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCTTGAGAGTGATCAGAAGGGCCTGCTGTGCG
AACACGAAATGCTTCCAGTAAGCAGAGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGTAATTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGTTGGT
GTGTGCTGTATCCCACTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAACTCAGTTCAGCCTGAGCACACAGCCGAGACTCTGTCTCAGA
AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLPKPDHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGACTGGGCGCCGCTTCGCCACTGGCCTCTTCTCTGGGAGGCGGT
GCCCCCATGGCGAGGCCGCGAGAGCAGTGCTGCTTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCAAACC
TGGCGCGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCTTGAGACCCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGAGGCATCTCGCCGTCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTGAGGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTIONCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCTGGGAACCCAGGAATTGAC
CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRRLKPAETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVVRVYIS
LLPLGDGLTIAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGAGCCGCTACCGCCGCTGCAGCCGCTTCCGCGGCCCTGGGCTCTCGCCGTCA
 GCATGCCACACGCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCCTCAC
 TGGCTGCCAGGATCGACGACATCGCGGATGGCGCCCTGAAGCCCCACCAACAAGTACCC
 CATCTTTTCTTTGGCACACAGAAACAGCCTTCTGGGACCCAAAGGACTGTTCCTCTAG
 ACAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACAACCCCAAGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCGGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGCTCATGCCGCTCACAGCGTAAACGCCACAGCTGCCAGCGACGAGTGAGAGGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGCGCTAAAGATGTC
 GGTCTCGAAACGAGCCCGAAAGGCCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAAGCTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGGCCACCGAGGGGCCCTCTGGGGGACCGGAAAAAAGAA
 GGCGCCGTGAGCTCCGACTCCGACTCCAAGGCCGATTCGGACGGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGGTGCGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGACAGGAAGCCAGCGGAGAGCCTCTCCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAGCGGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCCG
 CGGCGCGGAGAGCAGGAGGAGGAGCTGCGGCGCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGCGAGCGGGCCAGCCGCGGGGAGGCTGAGCGGGGACGCGGCGGACGAGCGGGG
 ACGAGCTCAGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGT
 CCCCCGTCTCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAATCAGC
 GAAGAAGCCGAGTCTCAAGCAGAGAGCCCGCCAGGAAAGCTGGCCAGAAGGAGAAGAGAG
 TGCGGCGCGGAGGAGAAGCAAGCCAGCCCGTGAAGGTGGAGCGGACCCCGAAGCGGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAGAGCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAGGTCGACAGCCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTGCGAGTGACCTCTCAGATCCTCCAGAAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA
 GAAGGCAGCAGAAGCTTATACCCGGCTCAAGTCGCGGGTCTCTGGGCCAAGATCGAGGCGG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGAG
 GAGCTGGCCGGGGAGGAGGCCCGCCAGGAGAAGGCGGAGGACAAGCCAGCACCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG
 AGGAGGGTCGGGACTCGGAGGAGGGGCCAAGGTTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGACGAGCGCAGAGGGCACG
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCGGGGACCCAGGCCAGCCCCCGC
 CCGAGCTCAGGCTGCCCTCTCCTTCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGCTGTGGG
 GAACGCTGTGCTGTTTGTATTGTTCCCTTGGGTTTTTTTTTCTGCCAATTTCTGTGATT
 TCCAACCAACATGAAATGACTATAAACGGTTTTTAAATGA

10017527.12.1301
 10017527.12.1301

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDQFTPEKKAAPRRRGPVGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKKPPRGRKPAEKPLPKPRGRKPKPERPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTRRRSEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTCTCCTGGATCTTCCACCTTACCAACTGCAGATCTTGGGACTCATCAGGCTCAATAATTATATTAATTA
 ATCCACTTTGAAGAGAGACATTTGTTTTTCATCAGGAATGCTAATAAGATGAAAGACTTAAGGCCAGAGCCAGGA
 TTTTCACTTTTCTTCTGCTTTGATGATGCTGAAGCATGACCATTTGTGTTCTTCCAGTCACTGGSCACTTTGAAGCA
 AATATTCCAAGACTCAGACTAACCTACAAGAGTGGTGTCTTCAAAATAGCTGTATTCCTTTTGGGTCTCATC
 AGAAGGACTGGATTTTCAAACTCTTCTCTTAGATGAGGAAGGCCAGGCTGCTTTGGGAGCCAAAGACCACAT
 CTTTCTTACTCAGTCTGGTGTAGCTTAACAAAAAATTTTAAAGAGATTATTTGGCTGCTGCAAAAGAACGGGTGGA
 ATTTATGTAATTTAGCTGGGAAGATGCCAATACAGAAATGCAAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCAATATGTGGGTATATTGATCTTTGGAGTCTACAAGGA
 GGATATTATATTCAAACCTAGACACATAATTTGGAGTCTGGCAGACTGAAATGCTCTTCGATCTCTCAGCAGCC
 TTTTGTCTCAGTAAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCGATTTTCTTGGCAAGATACCTGCATT
 CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTTGGAACCTTTCTTCATACAGACACCTTACAATCCAGATGATGATAAAATATATTCTCTTTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
 AGGAGGACAACGCGCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTTGTCTCAATTCCTGGAG
 TGATGGGGCAGATACCTTACTTTTGTGAGCTTCAAGATATTTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGAGCTTTTAAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCGATGATGGGAGAAAT
 TCTTTATTCACAGGGCTGTACATGTCCAAGCAAAACCTATGACCCACTGATTTAAGCTCCACCGAGATTTTCCAGA
 TGATGTCACTCAGTTTTCATAAAGCCGCACTCTGTGATGTATAAGTCCGTAAAGCTTGCAGAGAGGACCAAGCTT
 CAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAAGAGATGGCCAGTACGA
 TGTAAATGTTTCTTGGAAAGACATTTGGAAGCTGTCTCAAAGTTGTGCAGCAATTCNAAAGAAAGTGGAAATTTGGA
 AGAGGTAGTGTGGAGAGATTGCAGATATTCAAGCACTCATCAATCATTTGAACATGGAATTTGCTCTGGAAGCA
 GCACAAATTTGACATTTGGTTCCGAGATGGATAGTTGCTCAGCTCTCTTGCACAGATGCAACATTTAGGGAAGC
 TTGCGCAGACTGTGCTCTGCCAGAGACCCCTACTGTGCTGGGATGGAATGACTGCTCTGATATGCTCTTAC
 TTTCAAAGAGAGCACTAGACGGCCAAAGTGTAAATATGGCGACCAATCCCCAGTCTGGGCAATGCCAGACAG
 CATTAGTTCATGAACTGCTGATCAAAAGGTGATTTTGGCATTTGAATTTAACTCAACCTTTCTCGAATATTTAC
 TAATCCCCAACAGCACTATTAAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGAGACTTGAACCCGA
 TGAAGAAATCATCAAAACGGAATTTGGGCTACTGATTCGAAGTTTGAGAGAAAGAGGATCTGGGATGTATTACTG
 CAAGGCCAGGAGCACCTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTATTGGAGATGACACAGATGGA
 AATATCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCAGGCTTGAGATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCACTGCTGCAACAGATGTGGCAGAGGGAGAAGCG
 GAGACAGAGAAACAAAGGGGGGCCAAAGTGGAGCAACATGCAGGAAATGAAGAAGAAAGCAATCGAAGACATCA
 CAGAGACCTGGATGAGTCCCTTAGAGCTGTAGCCACCTAGTCTTCTACTTAATTTAAAGAAAGAAATTCCTTACC
 TATAAAAACATTTGCCCTCTGTTTGTATATCCCTTATAGTAATTCATAAAATGCTTCCCATGGAGATTTTGGTAAAG
 CACAAGACAATATCTGAATTAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTGTAACCAAGTTT
 CCAAGAACAAATCTTGCAACAGCAAGATTAAGAATTTATCTAAAAATAGGGGGTTTACAGTTGTAATGTTTTA
 TGTTTGTAGTTTGGAAATTTATTTGCATGTAAATAGTTGAGCTAAGCAAGCCCGAAATTTGATAGTGATATAAGGT
 GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTTCTTATGGAACCAAGCTACCTTTGTGTAGGGAATAAGAGGTGACACACAAATTAAGACAACTCCCATATC
 AACAGAAATTTCTCATGAGCAATTCACCTCTGGAGATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTTTCT
 TGGCCACTGGGGTTAAATTTAGTGACTACAACATTTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
 ATTGACTAGTACGAGATACACAGTTTACAGAGAGAAAGTTGTTGCTAGTTAGTTGTTTATAGATATATACAA
 GCTCTACAGGGAAGAATGCTTAATAAATACTTTAATAAGATATGGGAAATATTTTAATAAAACAAGGAAGAACAA
 TAATGATGATTAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAGACAGAGGAAGACAGGCAT
 AAATTTCTGGCTTTGGGAAACCTCATATCCCATGAAAGGAAGAACAAATCACAATAAAGTGAGAGTAAATGTA
 TGGAGCTCTTTTCACTAGGATAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATATAACAA
 AACTGTCTAGCAAAATCTGAGGAACACATAAATCTTCTGGAAGATCATAGGAAGAGTAGACATTTTATTATAAC
 AATGATTTTACGATATATTTTCTCTCTTAAAAAATATTTATCATATCTGTATATTTCTGTATATTTCTATGCTG
 TTTTATCTCTCTGTATATTTGATTTTGTGATTATATTTGAGTGAATAGGAGAAACAAATATAACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTGTTGAATAACAGACGAGTGTAAATTTTAAAC
 AACGGAAGGGTTAAATTAACCTTTGACATCTTCACTCAACCTTTTCTATTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTGTTTTGTAATTTAACAATAAATAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLLLDDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNKAKFIGTFF
IPDTYNPDDDKIYFFRESSQEGSTSDKTI LSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCC LARDPYCAWDGNA
CSRYAPTSRRARRQDVKYGPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTNL
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

CACTACCTCCCTGAGCCACTACTGAGCTGGAAAGCCGAGAGTGGCTGGAGCACTGCCAACCGGGGAGGAGCAG
CACTCCCCAGGTAAAGCTGGGAGCAAGCACTGAACTGTCTTCAGGAGCTGGGTATTTCCCTCCCAACCCCA
CTCAGCAAGCTTTCAAGCCAGCAGGACATGATCAGTGTGTGTCTTGGAGTGGGGAGCAAGAGCCCTGGCTGGCAACA
TGTCCTGGAGAAAGAGGTTTCAGCGCTTGACACCCGAGCTGCCCGTGTACATCAAGATCCAGAACCACTGGGCAT
GGGTGAGGTGGGGGGGACAGGTGTATGTGCACCTCTTGTCTCAGCAAGAGAGCTGAGAGAGGGGATCTTTGG
AGCCATTGAGGTTGAGCTTAGGAGTCACAGGGGGAGGAAAGATTTTAAAGTAACAGTGTGGCACAATATGTTAA
GAGCAGAGTTTTTGGAGTACAGACGATAGGTTCAAACTCTCTGTGTCTTCCTAGTTTCTGTAGCCCGAGGT
AAGGAGAGTCACTAACTCTCTGCAGTTCAATTTCTCATCACTAAAGTAGGGCCCAATAATAGCACCACCTCAT
AAGGAAGATTTAAATGACATAAATGTATGTATGCTCAACTAGCAAAAGTACCAAGTCCCATATAGTCACTGCCCA
TATTTTCCACCACCCTCTGTCTCTGCTTCCCAACAGGTAATGCACACAGTGGAGCAGAGGCGGCACAGGCTTT
CAGAGCGGGAGGCTTCAAGCACTAGAAACAGAGTTTACAGGAAGTCGCAAGAGACATCCGCGCGAGCAAGTGAAGCC
AGGTGAAGGGGGCTGCCGGCTGGCCCTCTCTCGAGGGGGCTGGCTTATAGTGTGGAACGCTGGCTGAAGCCACCTTC
TGACCCAGCCCGAGTGAAGTGAAGCAGAGCGCGGCTCAGTAGGCTGGCTGTCCGACAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGGTTTCTGCACTTTGAGGAATGTGAGGAGCAGCGGAGCTCTTTGAGGAGCTTGCCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTTGCCTGCACAGTGAGTTATTCGTAATAGCAGGGGCTGAGGATGT
AGCTGACAACTCAGGAGGCTGAGTGGCTGAGGATGTACAGAGAGGGAGATGCTGCAAGATGGGTCAAGGCTCGGA
ACACGACGCGGAGAGTAGGCTTTGTCCAGGCAATATCTCAACTTCCCGAGTCTCTCTCCAGAGAGCAACCC
AAGACAGTGACAACTCTCGGGGACAGCCACAGCAATCTCTGGCAAGGCCCTGTACAGCTGACAGCCAGCA
GTGACAGAGCACTGAGCTTCCCTGAGGGGCACTCACTCCGTCTGCTCGCGGGCCCAAGTAAAGATAGATGACG
CACTTCTGAGAGGGAGATTTTGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGAGAGAGTCTGCTGGCCCC
CAGGCGCCACTGTGATCTCTGCACCTGAAAGAGATGTGCGCTGCCCTCTCTCTCCAGGCTCTCTCCCACTGCACT
CTAGGCTTTGGATGGGCCCTCGACCTGTCTGTCTGGGACAAAGCCGATCTCCTGGGTTCTCTGG
ACATGATGGCACTCTGCACTCAGCCGCAATGGTCCACCACTTCCCGCGGCTTAAAGCCGCCGATCTGGCCAC
CGATCCCTCACCCTAGAGGCCAGGAGGAAGCTGACCCCAAGTGAGTGCTGTCTCCCTATCTTCAAGCTGTGAGA
CCACCACTCAATGATCCAGAGCAACAGCAAAAAGCTGGAATCGCCCTTATTTCCACCTCACTCCAAAGGT
GGAACCTTGCCTCTCCATTTCTAGAGCTTACAGAACCACTCTTTTTCATTTCTATCACTCTAGGAG
GGAATCACTACCTTCTCTCTGTATGACCACTATCTAGGGTGGTGAATTCCTGAATCTCTGGGGCTGAAACC
ATCCTCAAGTCTCTAGTAGTTTGTGCCCACTCTTTCCCAACCTGGCTCCTGACCAACCACTCTCGGATG
CCAGGTCAGCTGGGTTGGGCTGGGAGAGGAAGCAAGGCTTGGGAATCAGGAGCTGGAGCCAGGATCGGAAGAG
CTGTAAATGCTCAGGCAATTTTATGCAATGAATAAAGGCGCAAGGCGAGCCAGGCGCTGGGCTCTTTGTG
CTAAGAGAGGCGAGGGGCTACCGTGTGATTTGCTTTAGGGGCGCAACCGGCGAGGGGCTGTCCTCCAGCTGCCAC
GCTCTATCACTGAGCAGAGTTGTGGGAAAGCGGGGCGAGCACTTGTGCAAGCTGGGCAAGGAGCAAGAGAC
TGAGGGGCTGTGACCTTCTCAGGCGCCAGGCTGAGACTGTGCAACTCAAGTGAAGTAGAGCTGTGCTCT
AGCTGGGGGAGTGCTGTGCTGGAGGGGGAGGGCTTTCAAGCCCAACCCCACTGGCCCTGGCCAGTGGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAGAGGAGAAATAAACAATGTGTCTCTTGTCAAGCTGTGCTCGAG
TTTTCCCTGGGGCTCAGGACCTTCCCTAGCTCCACAACCAAGGAGTTTATAGCAAAAGGCTAGGCTGCG
AGTTTATCTCGGGGCTCAGGAGGCGAAGAGGCTTAAATAGTTTAAGTAGTCACTGGGAAGTCAAGATTAACCTCA
TTTAGGCTGAGGACACTCACTCACTACTCTCTGCTTGGTGTGAGAGACACTGAGACAAGAGGAGGGG
TCAACAATGAGAGACAGAGATAGTCTTACTGACCTGCCCGCAGAGTAGAGAGCAATAAGACGCCAGCCAGCTG
AGTCGGGCTGTGTTTCTTACTGGTGAATCAGAGTGCTGTGGTTGCTTGGCTGCCATTTGCTCTTGAAGTG
GCAGCCTTGGGCTTGGGCGCTCTCGCTCGCGCTCAAGTTGTTGGTCTCGAGAGCTCTGGGGTTCTCTCAAGTG
CAGGAGGGGTTAGGCTGTCTGCTGCTGAGTCTCCATTTCTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC
TCTCAGGGGAGCACTCTCCATGCGAGCACTCCCTGCTTGGGCTGCCCTCCCGACACCCCTGACACACCCCTG
GGTCTCTGCCCAACAGAGCCCAAGCTCTGTGTGGGGGAGCAATCAGGTTCTGTGTGCTGACCTCATAGGCTCT
TCTCAAGTGTGTGCACCGGAAGCTGGGAGGGAGGAAAGCTGGGTTTAGGACCAACTCAGAGGCTGCTTGG
GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGTCTTCTCTGCGCTTAGGTAAGGAGGAGCTCTC
AGATTGGGGACATTTGTGTAGCTGACTTGTCTGGAGCTCCAGTAGGAGGAAGAGCAAGGCCAATTT
TTGGGATCAGTGTGCTGATCACTGGGCGGCTCACTCAGCCCGGCTTCTCCTGGAGCACTGCCCACTGCCCA
CAGAGAACACAGTGGTCTCCCTGTTCGGGGGCGGCTTTTTCCTTCTTGGAGCGTCCCTGACGGACAGTGAAG
GCCCTCTCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGATGATGGGAGGGGCTCT
CGTCTGCAGGCTGGAGTGGCATCCACATGGACAGCAGGAGGGGAGTGAAGGTAACTTTCAATTTCCCT
TCATGTTTGTGTTCTAGCTTTCTTCAGCATGCTCTTAAACCCCAAGAGCCCAATTTCCCAAGGCCCAATTT
TTTTCTGCTTTTATCAATAAATCAATATTAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDAEELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFVRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWGEFGGRVGVFPPSLVVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSLVDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGACCGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCCACAGCGGAA
 GAGGGCAGAGACAGGGCAGGCACAGAGCGGGCCACAGACAGAGTCCCTACAGAGGGAGAGGCCACAGAGAGCTGCGAGA
 AGACACAGGCGAGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAGACCCAGACCCCTGG
 GCACCTCTCCCAGGCCAAGGACTAAGTTTTCTCCATTTCCTTAACGGTCTCAGCCCTCTCGTAAACCTTTGGC
 TCTGACCTTTGGCAGGAGTCCCAAGCCCCACGGCTACAGAGAGGAGCTTCCAAAGCTATAGGTTGTGGAGGACTTGGT
 GCCTTAGACGGCTCAGTCCCTCCAGCTCGAGTACCACTGGCCATGTCACAGACAGGCTCGCATCCCGGGAGGAGAGAT
 CTGGGACGGGCGTGGCTGTGGGAGGCCAACCCCTGCCCTCCTGCCCCATTGTGCCCTCTCCTGGCTGGTGTG
 GCTGCTTCTGCTACTGCTGGCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCTCCCGGGAGGAGAGAT
 GGTGTTTCAGAGAACTCAACGGCAGCGTCTGCTGGCTGGGCGCCCTGCCAGGCTTGTGTGCCCTTGA
 GGCCTTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGACAGGTGAGGGGCTGACAGTGCAGTA
 CCTGGGCCAGGCGCTGAGTCTGCTGGTGGAGCAGAGCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTCTGCATCGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACATCCA
 CCTCCAGCCCCGTGGAGGGAGGCCACCCCTAACTCTGCTGGGGACCTGGGGCTCAATCCTACGCCGGAAGAGTCC
 TGGCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCGGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAAGTGGCCGATTCCACGGTGC
 GGGGCTAAAGCGCTA CTTGCTAACTGATGAGCAGCAGCAGCCAGGCGCTTCAAGCA CCGAAGCATCCGCAATCC
 GTGCAGCTTGGTGGTGA CTGGCTGATGATCTGGGGT CAGGCAGGAGGGGCCCAAGTGGGGCCAGTGTCTGC
 CCAGACCGCTCGGCAGCTTCTGTGCCCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCTGGGCCCTGACCACTTTGA
 CACAGCCATTCTGTTTAACTCCGTGAGCCCTGTGTGGAGTCTCCACTTGCACACGCTGGGATGGTGTATGTGGG
 CACCGCTGTGACCCGGCTCGAGGCTGTGCCATTGTGGAGGATGATGGGCTCAGTGCAGCTTCACTGCTGCTCA
 TGAACCTGGGTGATGCTCTTCAACTGCTCCATGACAACTCCAAGCCATGCATCAGTTTGAATGGGCTTTGAGAC
 CTCTCGCCATCTCATGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT
 CATCACTGACTCTCTGCAAAATGGCTATGGCAGTCTCTTGAAGAACCAAGAGCTCAATTCAGTCTGCGCTGT
 GACTTTCCCTGGCAAGACTATGATGCTGACCGCCAGTGGCAGCTGACCTTCGGGCCGAGTCAACGCCATTGTCC
 ACAGCTGCGCGCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGAGCATGCCATGTGCGAGACCAACA
 CTGCCCTGGGCGCCATGGGCACACCTCGSGGGCCCGCACAGGCGCTGCATGGGTGGTCTGCTGCTCCACATGGACA
 GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGGTCTTGGGAGCATTGGGTTGATGCTCTCGGACCTGT
 TGGGGTGGTGTCCAGTTCTCTCCCGAGACTGCACAGGCGCTGTCCCCGGAATGTGGCAAGTACTGTGAGGG
 CCGCGCTACCGCTTCCGCTCTGCAACACTGAGGACTTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
 GTGTGCTGCTACAAACACCGCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCTCTGCTACAC
 AGGCGTGGCCCCCAGGACCGATGCAAACTCACCTGCCAGGCGCGGGCACTGGGCTACTACTATGTGCTGGAAGC
 ACGGTTGGTAGATGGGACCCCTGTTCGCCGACAGCTCTCGGTTCTGTGTCCAGGGCCGATGGATCCATGGCTGG
 CTGTGATCGCATCTTGGCTCCAAAGAGAAGTTTGACAAGTGATGGTGTGCGGAGGGGACGGTTGTGTTTGAG
 CAAGCGCTCAGGCTCTTTCAGGAATTCAGGTACGGATACAACAATGGTCACTATCCCCGCGGGGCCACCCA
 CATTTCTGTGCGGAGCAGGGAAACCTTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGTGTGCTCCTTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGCGACTCAGCTTGGCGTA
 CAGCGGGGCACTGCAGCCCTCAGAGACACTGTGAGGCCATGGGCACTGGCCAGCTTGTGACACTGCAAGTCTCT
 AGTGGCTGGCAACCCCGAGGACACAGCCCTCCGATACAGTCTCTGTCGGCCGCGCCGACCCCTTCAACGCCACG
 CCCCATTCCCCAGGACTGGCTGCACCGAAGAGACAGATTCTGGAGATCCTTCGGCGCGGCCCTGGGCGGGCAG
 GAAATAACCTCATCTACCCGGCTGCCCTTTCTGGGCAACCGGGGCTCGGACTAGCTGGGAGAAAGAGAGAGCTT
 CTGTGCTGCCCTCATGCTAAAGACTCAGTGGGAGGGGCTGTGGGCGTGAGACTTGCCCTCCTCTCTGCCCTAAT
 GCGCAGGCTGCCCTGCCCTGCCCTTCTGCTGCCCTGGGAGCAGTATGGTTAGTGATGGAAGGGGCTGACAGC
 AGCCCTCCATCTAACTGCCCTCTGCCCTGCGGGTCAAGAGGAGGGGGAAGGACAGGAGGGGCTGGGGCC
 CAGTTTGTATTATTAGTATTATTACCTTTATTAGCAACAGGGAAGGGACAGGACTAGGGTCTTGGGGAA
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGTATATAGTGGT
 TGTGTATCGGTGTGTGGTGTGTGGAAATGTGTGTGCTTATGTATGATCAACCTGTCTGTCTTTCTCCT
 TTCCTGAAATTTATTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCTTCAAGGATGAGGATATCTTTT
 TTTTTTTCTTTCTTTCTTTCTTTTCTTTTGTGAGACAGATCTCGCTCTGCGCCAGCTGTGAGTGCAATG
 GCACAACTCTCGGCTCACTGCACTCCCGCTCCCGGGTCAAGTGATTTCTCATGCTCAGCCTCCTGATGAGTGC
 GGATACAGGCTCTCGCCACACCGCCAGCTAATTTTGTGTTTGTGGAGACAGACTCTGCTATTTGTGTC
 ACCAGGGCTGAATGATTTCAGCTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATCTCTGCTCCCTGAGCCTC
 CGAGTAGCTGAGATTATAGGCACTACCAACCGCCGCTAATTTTGTATTGTAGTAGAGACAGGTTTCAACGT
 CATGTTGGCAGGCTGTCTGCACTCTGACCTTAGGTGATCCACTCGCTCTCATCTCCAAAGTGTCTGGGAT
 ACAGGCTCAGCCAGCTGCTGCCACGCCCACTAATTTTGTATTGTAGTAGAGACAGGTTTCAACAGT
 TGGCCAGGCTGCTTTGAACCTGCACTCAGGTATCGACCTGCGCTCCCAAGTGTCTGGGATACAGG
 TGTGAGCCACACGCGCGTACATATTTTAAATGAATTTACTATTATGTGATCTTTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTCTCATTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTGAGGATTAATTAATGTAATAAAGAACTAGCATACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAGGAAA

FIGURE 180

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNQSVLPQSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTTGTINGDPESVASLHWDGALLGLVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPNCNVKAPLQSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVTVLVLGSGEEGPQVGPSSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSTRHCPQLPPCAALWC SGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLEHMDQLQDFNI PQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRDTLFSFPGMPDWVPRYTGVAPODQCK
LTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFKDKMVCVGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVLPGAVSLRYSGATAAETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFVPRPT
PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAAATATGTAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
 AATTGTCTGTTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATCCAAAATCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACCTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGAAGAAGAACTTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TA**AGGAGGTTTGAGCTCAAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRNRNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWW
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAC TGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCTGCCGACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCGCCCTCATGTCATCTCTGCTGCTCTCGGGCATAGCCT
 GCGCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCTCCTGTGCATGGTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCTGCTTTGCCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAAACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCACAGCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATAACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCAGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTCAKGTFAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSIGGTLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTTCAGGCTTCACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGC
 CATGCTGCAGGAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCCAGACCAGGTACACATTGGTGCGGCTCTGTTCTGTG
 GGTGGGTGCGTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTGT
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACCAAAAAACAAGAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGGGCAACCAAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGCTCAGAAATGTCCCTAGATGAATGAGAAAAATTATTTTTTTTAA
 TTAAGTCCTAAATAGTTAAATAAAATATGTTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATATTTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAAGTTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCCTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGAACACAGCAAGTCTAGGAAGTAGGTTAA
 ACTAATCTTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGATGTTGGTGC
 TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGC
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTGTGTATGTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGCTGTCATCAGCTATTTATGATTCTATAA
 GCTATTTACAGCAGAATGAGATATTAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGTGTTCAAGCATCTACTCTTTTTATCATTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGTTG
 AAGAAGGTTACTATTAATTGTTTAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA
 AGATTAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAATAATTAACATTTTTAAACGCAGATATTTGTCAAGGGGCTTTCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCCTTTGAGAAGCTTCACTGCTCCTATGTGGGTACCTGAGTCAAAATG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTAGTTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTTTATCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTAATAAATTGTACATTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TGCC**ATG**GCCTCTGCCGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGTTGTGGGAGGGCCCTGTGGATGTCTCGTGGTGCAGAGACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTACCTCTGGGA
TTGTCTTTGTCTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGCGGCCCTCAGGCCCTTTGTGCTGGGTGGGGGTTGCTGTGCTGCATCT
GCCCTCTCGGGGGGTCCAGGGCCCGAGCCATTACATGCGCCGCTACTCAACATCTGCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGA**CGTGGAGGGGAAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTTTCTGCCTCCTGCTATTTTTCTTTTGAAGGATATTTAAATTCATT
GAAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAAGTAATGCGGAGGCTGCTTGTGCTGTGGCTTTGCAACAAGACAGAC
TGTCCTCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCTCGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCTCCGTCCTGATAAGACG
CTCCCTCCCGAGGCCAGGTCCACGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
TCTACTGCCCTGAGGCCCTCGTCTACCCCTTTACACTCACATTTTTATCAAATAAGCATG
TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSI VVAQVVWEG LWMSCVVQSTGQM
QCKVYD SLLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGQPSHYMARYSTSAPAIRGPPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATATCCC
 TTGCCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGACTCTTGCCACAACCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCA
 GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGGAGTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGCTCTTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTAAATGCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTATAAAGTCCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
 GAACCTGCTTTATGTCTAGATTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAATTGATATTCTATAACAATAAACATATACCTATTCTA

1007567-1234567

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**CATG**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCTGCCCCATCA
CATACCTACCACTTTGTGGTTCTGACTACATCACCATATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
AGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCATGCCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSSEAAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATGG**GCTGCCTCCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTACAGAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLLCWGPGGISGNLKLMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCCGAAGTGCCTGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
 CGTCTCTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTAGGGACCCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCAGGACTCCCCGAGGAGCCCCCTCGTGCTACGGGTGAAATTCCTCAATGATTACAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCCCGCGGGGTCCGAGCCCGCCCCCTCCGGGCTGGAATTCGGCAGCCT
 GCTGCTGCCCCTGCTGCTCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCTGCTCCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
 GGACCTTGCTCCCGCGCGCGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
 CCCCGCCCTGCGACCGCGCGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCCTCGGGGTGGGCATCTGCTGTCGCTGCCTCGGCCCGGGCAGAGCCG
 GGCCGCCCGGGGGCCGCTTAGTGTTCTGCCGAGGACCCAGCCGCCCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGAG
 GGGCAGAGGAGTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLFPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPCCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGACCCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTACAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCCACACGC
 TGTTGGCAATGTGAGGACCAAGTTAAGTGACTGGCAGAAAACCTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTTAACCTGAACATGAC
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCCTCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCTGCAACGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAAGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCTCATCAAGCAGCCAAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAAGCTGGACCCAC
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGG
 CACCCACTGTGCTGCAGCAGCCCTCAGGACAGCCTGCCACAGCCAGCCTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTGAAGGAGATCATCCTCGTGGAGCAGCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGGACTGGAAGCTGGATTTTCACTGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGCCATGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGTGGTGAACCTCGAAGCTGTCTTCAAGGCCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACAGTGCAAGGAGACTGGGTGTGCGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGACATCTGGGCT
 GTCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTACATTTGGCAGCCCCAGCAGCACTGTGCTTGTGTCAGGCAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCGTGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTTCTTTCTGGGAAATGCATGGAAGCTGTGGTCAAGAAAAAC
 AATAAAGATTGTACTGCGTCCGTGTGATGGAAGCCCGCCAGCAGTGGCGATTGGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGCAAGGAGAAAAGAAATTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATTTTCAAGCTGATGCTCTTTGTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAAGATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
>subunit 1 of 1, 639 aa, 1 stop
>MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIIYQNQDSHSPLDQEATL
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLGCRTHFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCFMVLAPCSDSRQQYQLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCTCTCTGGCCACTGCTGTTGTC
 TGCCCTCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCTCTGCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCCG
 ATTTCTGGACTATGTTTTCAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGAGGCACCTGCCACCTTGGGCGCATTC
 CTGTTGCGGGGGCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGAGCCAGAAGC
 GACGCAGACCTCAGGCGAGCAAGGTGCCCTGAGGAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCGCGCTGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGGCAAGGGGAAGGCAAC
 TTAGTCTTTCAGAGCTGGGGTGGGGTGCCCTCTGGATGGGTAGTGAGGAGCGAGGCTGGC
 CTCCACAGCCCTTGCCCTCCCAAGGGGGCTGGACCAAGCTCCTCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTTGCCC
 TCTTTGGTTTTTTTCTCATGCCACCTTGCTAAGACAACCTGCCCCCTTAACTTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCCGAACACTCCCCAGCC
 CCACGGGCAATCTCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCTTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
 AGGCCATTTCACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACTTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
 TGTGCGGCGTCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGACGCCCCGTC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATGG
 TCTCTCCATCCACACCATTTGTTTCTCTGCTCTCCCATCCTACTCCAAGGATCCGGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCAGCCCA
 CTGCTAAAATCTGTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTGTCTGCTGCTGGCTG
 TCTGTGTGTGGCCATCTCTGGACTTCAGAGCCCTCCTGAGCCAGTCCCTCCCTCCAGCCT
 CCCTTGGGCTCCTTAACCTCACCTAGGCTGCCAGGACCGGAGTCACTGTGTTTCAAGGCC
 ATCGGAGCTCTGCCTCCAAGTCTACCTTCCCTTCCCGGACTCCCTCCTGTCCCTTCTTT
 CCTCCCTCCTTCTCTCACTCTCCTTCTTCTTGTCTCCCTGCCCCCTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGCTTTTTCCACCTTCTCCTTCCCTTCTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGATATCTCTTCTCTCTTGTGGTGATCATTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRITSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCTGCGCTGAGAAAGTTTTCTGCCTCCT**TGA**AGCGAATAAA
GGGGCCGCGCCCGCGCGCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVA PGPE DSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GCGCGTTGGTTGGTGGCGGCTGAAGGTTGTGGCGGACGACGCTCGTTGGTTGGCCGGCG
 CGGGCCGGGACGGGC**ATG**GGCCCTGCTGCTGTGCCTGGTGTGCTGACGGCGGCGCTGGCCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTTACCGCCACCATGTGA
 ACTTCAAGTCTCTGGTGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCAGCTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACC CGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAA
 GCCATCATCGAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGGAGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GATGCC
 CCAGAGGCGCTGGGAGTGTGTGCCACCCCTCCCTCGAAGTTTGTCCATCTCAGCTGGGG
 GTCACACCTGGGGACCCCTTCCCTCGGGCGCTGGACACACATACATGAAAACAGGCGGCAT
 CGATGTGACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG
 ACTCGCAGCTCGCTTGTCTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC
 CTGGCTGTCTATCGGGTAGGGCGGGGCGGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT
 CCCACAGGTCTCTGGCGCAGTGGAACTCAGCTGTCCAGGGCCTCCTGAATACATAAAATTAAC
 TGGCACAAGTAAGTCCCCCTCTCAAAACCAACACAGGCAGTGTGTGTATGTGAGCACTCGTG
 GGTGAGTAATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTCTAGAGGGGCTCCCGA
 GGAGTGGAACCTCAACCCAGCTCTGCGCAGGAGGGCGGTGCAGTCTCTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGGCGGGCATCTTCTTAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCATCCAGGTCTGTGTCAGAGCCTGGGAGGGTTCCCTACGATGTTTAGGGTGCCCC
 CTGAGGGGGCTGACTCGCCCAAGTATGGCTTTAGACAGGACGAGCATGAGGTAAAGGCGCG
 AATGACCTGGGACTTGGGGGAGGGGGTAAAGGAGAGAGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
 CCTGGGACACACAGAGCCACCCCGGCTTGTGAGTGACCCAGAGAAGGGAGGCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTCCGCGGCCTGCACACCTTCGGACATCCCAGGC
 ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCCAGCTGGGAGGAGAGGGCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAGATGCTGCTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
 GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCTGTGCTACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGATCCCCCTCTCCGACCTCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGGGAGG
 GAGGATTAAGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAAGTCCGAGAGCTGCGGGA
 TGTGATTAAAGTCCTCATGTTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAAGTTGCTGCAGAAAGTTGAGAAATCCTCAGATGGTCTGT
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACCTAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCCACACACACACGACGTCACACACGACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAATCTCGTTTTTCTC
 TTCTTCTCTCTTTTAAATTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGTCTTTTAAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
 ATGGTTTTAAACACCTTTGTGAAATGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAAATAAAAGGAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEEVEKSSDGFGAAQEPTWLTDPVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRILDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTYENPVTVIGLFNSVIQIHLLIMNKASPEYEEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVSEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCTGCACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATC
CTCAGCAAGAAAACAAAACAAACIGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTGTACTTTCTTTTC
AGGTCAATTTACAATTGGGAGATTTAGAAACATTCTTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTCTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
AAATGTGTCATATCAATTTCTGGATTCTAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCATTTCAATCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASININ
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGTCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

CCCGGCTGTGCAGAGACGCCA**ATG**TACCGGCTCCTGTCAAGTACTGCCGGGCTGCCGCC
CCCGGGGGCTTGGCCTCAAGTGTGGGACGACGCGGGTCCATCAGCGCGCCGGGCTGCCGCC
TCTCGGCCACGGCTGGGTCTGGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCTCTGGGGTGAAGC
TGGCAGGTGGGGCTAGGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCGGACCTGAGGCG
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGAGACCCCGGC
GCCGCCCTGTCTCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACC GTTACCATTGTAACACAGAGACAGT
TATGCGAATTGCTAGCATCAGCAAAAGTTCTCACCATTGGTTGCTCTTGCCAAATTGTGGGAG
CAGGGAATCTGGATCTTGATATTTCAAGTACAACATTATGTCTCCCGAATCCCGAGAAAAGAA
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCAATTTAAGTGAATTCG
TCATTATGAAAAGGACATAAAAAAGGTGAAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
AAAGAATGATTTTGAACAAGCGCAATTTATATTTGAGAGAAAAGTTTGAAAATTC AATTGAAT
CCCTAAGATTATTTAAAAATGATCCTTTGTCTTCAAACCTGGTAGTCAGTTTTGTATTCA
ACTTTTGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTTGGA
CTATATGCAGAAAATATTTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTTACAATAGAGCAAGGT**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
TTAACACTGATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
CACATTTTGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAAACA
TGTTTATAAAGTAAAAAAA

FIGURE 214

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
>subunit 1 of 1, 373 aa, 1 stop
>MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPSCSRCFARAIESRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEKEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLETTVQENEPVIYNRR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGTCGAGAGGGCGAGGCCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCTGTCAAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCGGACCACTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTGCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCTCTGTTCCCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATCACTGCTCACTTGATACGTTATTCAGAAACCAAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQDGTLSLSQRQLSEEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTGCTCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGTCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAT
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGCCTGCAGCAATCCCTCCTTCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTACAGTCTCTTTGGCCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGTGCTAGTGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGCGACGCGCCG
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCACTTTCATCTTTGTCTTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGCTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAACACATTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFNNHVLAVVAG
VAAEAVASWIGLGPVAPFVAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLTGIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFISCSAVMMALLAVVGLFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGCGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTTAAAGAGCTGGTGGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
```

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRTHDYL FQVLSPGDIRYIF TATPAKDFGGIFHTRYEQ
 IHLVPAEPPEACGELSNGGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAV IISDNAVDNDSF
 YVEMIQDSTORTADIPALFLLGRDGYMIRRSLEQHGLPWA IISIPNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQCGGIYKDNNKSSIHCMDLQRYCLMAVFNVVYLENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGCGATGTGGAG
 GGTGCCCCGACAAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
 CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCACCTGGGCAGGGAAGATGTAT
 GGCCCTGGAGGAGGCAAGTATTTAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
 GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
 ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATAC
 ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
 GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
 AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
 TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
 AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
 GTGGTGGTGGCTGATGGTACTGGAGTAAGTACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
 AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLITYSANSFVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACCTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCGTGGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTGTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTCTCGGTGTGAGCGACCTGACTACTACAGTGCAGCTG
 ACAGGGGTGTCTGCAACTGGCCCCCTAAGCCAAAGCAAAAGACTAAGGACGACCTTTGAA
 CAATACAAAAGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTCTCTGCGCAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGTATTAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGTCAACCCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCCTTAGTTCCAATAGAA
 TCTCCTATTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGCGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCGAACTCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTTATCTGTGCCAGTCCCAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAATACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAAGCAT
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGTTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCGAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACAGGAGACCGAGCAGGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
 TGAACCATTTGTGATAAAAGAGCTCTTAAAGCTGGGAAATAAAGTGGTGCTTTATTGAACCT
 TGGTGAATATCAAGGGAACGGGATGCCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTCTGTCCGTTTTAGTGCATTATAAATACTGGTCATTTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAACAATCAATGTGAAGCTTGAACCTCCGTTTAAATATA
 TACCTATTGTATAAGACCTTTTACTGATTCATTAAATGTGTCGATTTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAAATAA

FIGURE 226

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAG
CLGLSLRYSNLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELISSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRITIPVRIFQDCRNLELL
DLGYNRIRSLARNVVFAGMIRLKLHLEHNQFSKLNLLFPRLVSLQNLQWNKISVIGQTM
SWTWSSSLQRLDLSGNEIEAFSGSPVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTC TGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAATATGTC AAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTCGCCGTATTCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCCTCAGTGTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCCACCATGGCAGTTTTTGTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCCTGTCCATGTTTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTTCGACAAAAGATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCATATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGGCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTGTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDCMVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCGAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAAACT
 CCCTCTTCAAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTGGACTCATT
 TGGGATTGATGTTACTGCATATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAACTACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAAATAAAGAACGAATCTCTCGGGCAGTATCAGATAGCAGTTGAAAAATCACCTTGTC
 TGCTCCATCCACTGTGGATTATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACCTTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCTATGAAC
 TCTAATTTCTGTACATAAAAAATTTTAAAGTTAATTGTTTGCTTTTCAAGGCAAGTCTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGTGTAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACATGAAAAACATGGATTC
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAACGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCATATCCTTCAGAATAACTGA
 AGGTTAATTATGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAATGGGTAG
 CAGCCACTGTCCATTAGCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAATAAGTGT
 GTAACCTCAATCTTATACTTATTGAAGAATAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTCACATACATGAATGTTCATTTTAAAGTTAATCCTTTGAGTGTCT
 ATGCTATCAGGAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGAAAGTGTTAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAAATTTGTATAACAGATGCATTAGATATTTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCATACTTGGGTAATTTCTAGTATAAAACAAATTTATCTTTTAT
 TTAATTTCCCTTGTAGCAAACTCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTTAT
 CTTATAGTAAGTGCCTTAAGTGCAGCTAGCTTCTAGATTTAGCATATATAGAAATTTAGATAT
 TGTATTGTTGCTCATTTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
 TAAATATGTGAATATTTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTCTCTGTGA
 CTGCTCACTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

[illegible]

FIGURE 232

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATCTACTGCAAGTGCTGT
 GTTCCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGCAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCCAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATGAGACCATACTTGATAAGATTTTGTAAATATCTT
 TCTGCTATGGATATATTTATTTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTTATACAGTAAAAAAGAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGGTTATTCAATTTGATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFFKTSFDISPEMSFSIYSLQVFAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACAGCTAGTGAAGGTTCAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTT**TAA**

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEH
YPLWKS VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYD TVKH YLV LNTPLEDNIMTHGLSSLCSGLVASILGTP
ADV IKS RIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCTCGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGAGGTATATTGTTTTTACAGGC
TGGTGGAATATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTATGTTT
TGAGTTTTGAAATAGTTTATGAAATTTCTTTATTTTCATTGCCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAAACCGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTGTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTCAAGTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCTCGGGTGAAGCTGACCCCAAGCCACCCCTTCACTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTATTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGCTCTGCCACGCTGGCTGGCA
 GCCTCGCCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACTGGGCTTCGGGGACAGTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGAAGGTGCTGCAGGTCCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGTGCTTTCGTGAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAATTTTA
 TTTTGTGCTGTTTGAATAAAAAAAAAAAAAAAAAA

100752724301
 100752724301

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKFLSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDNKNYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

Figure 6

Figure 6 consists of two panels, (a) and (b), showing the evolution of the normalized velocity autocorrelation function $\langle v(t)v(0) \rangle / \langle v^2 \rangle$ as a function of time t for different values of the parameter α . The y-axis ranges from 0 to 1, and the x-axis ranges from 0 to 10.

(a) $\alpha = 0.1$: The curves show a rapid decay from 1 to near 0 by $t=2$.

(b) $\alpha = 0.5$: The curves show a slower decay, reaching near 0 by $t=8$.

The legend indicates four cases:

- \square $\gamma = 0.1$
- \triangle $\gamma = 0.2$
- \circ $\gamma = 0.3$
- \times $\gamma = 0.4$

[illegible]

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGSPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPFPNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
FSTEEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLNKRKSVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$
[illegible]

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLLIHSFLPGGILPFSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCTCCGCCTCCAGCTCCGCGCTGCCCCG
 GCAGCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGT
 TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTCAAGACCTCTTCCCATGGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGCTCAGATTACCCAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTTTAAATTTTCATTTTGCTACCTCTTTTTTTATTTATGCCTTGGAATGGTTCATTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
 GGTTCATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTTGTAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

FIGURE 246

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHR TSSVEGLCEGIGAGLVDVAIWVGTCSDPKGDASTGWNSVSRITIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217